

TO 5 2 3 13

SEQUENCE LISTING

<110> F. Hoffmann-La Roche AG
MorphoSys AG

<120> Anti A-beta antibodies and their use

<130> F 2842 PCT

<140> EP 02003844.4

<141> 2002-02-20

<150> EP 02003844.4

<151> 2002-02-20

<160> 414

<170> PatentIn version 3.1

<210> 1

<211> 9

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; first region of beta-A4 peptide

<400> 1

Ala Glu Phe Arg His Asp Ser Gly Tyr
1 5

<210> 2

<211> 14

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; second region of beta-A4 peptide

<400> 2

Val His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly
1 5 10

<210> 3

<211> 368

<212> DNA

<213> artificial sequence

<220>

<223> synthetic construct; VH-region of MS-Roche#3

<400> 3

caggtgcaat tgggtgaaag cggcgggcggc ctggtgcaac cgggcggcag cctgcgtctg 60

agctgcgcgg cctccggatt tacctttagc agctatgcga tgagctgggt gcgccaagcc 120

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cctgggaagg gtctcgagtg ggtgagcgcg attagcggta gcggcggcag cacctattat 180
 gcggatagcg tgaaaggccg ttttaccatt tcacgtgata attcgaaaaa caccctgtat 240
 ctgcaaataga acagcctgcg tgcggaagat acggccgtgt attattgcgc gcgttcttact 300
 cattatgctc gttattatcg ttattttgat gtttggggcc aaggcaccct ggtgacggtt 360
 agctcagc 368

<210> 4
 <211> 122
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic construct; VH-region of MS-Roche#3

<400> 4

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val Trp
 100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 5
 <211> 379
 <212> DNA
 <213> artificial sequence

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<220>

<223> synthetic construct; VH-region of MS-Roche#7

<400> 5

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caggtgcaat tggaggaaag cggcggcggc ctggtgcaac cgggcggcag cctgcgtctg      60
agctgcgcgg cctccggatt taccttttagc agctatgcga tgagctgggt gcgccaagcc      120
cctgggaagg gtctcgagtg ggtgagcgcg attagcggtg cgggcggcag cacctattat      180
gcggatagcg tgaaaggccg tttaccattht cacgtgataa ttcgaaaaac accctgtatc      240
tgcaaatgaa cagcctgcgt gcggaagata cggccgtgta ttattgcgcg cgtggtaagg      300
gtaatactca taagccttat ggttatgttc gttattttga tgtttggggc caaggcaccc      360
tggtgacggt tagctcagc                                     379

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<210> 6

<211> 126

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; VH-region of MS-Roche#7

<400> 6

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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1           5           10           15

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20           25           30

```

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Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35           40           45

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Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50           55           60

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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65           70           75           80

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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85           90           95

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Ala Arg Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr
100          105          110

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Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115          120          125

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<210> 7
 <211> 374
 <212> DNA
 <213> artificial sequence

<220>

<223> synthetic construct; VH-region of MS-Roche#8

<400> 7
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 agctgcgcgg cctccggatt taccttttagc agctatgcga tgagctgggt gcgccaagcc 120
 cctgggaagg gtctcgagtg ggtgagcgcg attagcggta gcggcggcag cacctattat 180
 gcggatagcg tgaaaggccg ttttaccatt tcacgtgata attcgaaaaa caccctgtat 240
 ctgcaaataga acagcctgcg tgcggaagat acggccgtgt attattgcgc gcgtcttctt 300
 tctcgtgggtt ataatggtta ttatcataag tttgatgttt ggggccaagg caccctgggtg 360
 acggttagct cagc 374

<210> 8
 <211> 124
 <212> PRT
 <213> artificial sequence

<220>

<223> synthetic construct; VH-region of MS-Roche#8

<400> 8

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

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Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Val Tyr Asn Pro Pro
 85 90 95

Val Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
 100 105 110

<210> 11
 <211> 330
 <212> DNA
 <213> artificial sequence

<220>
 <223> synthetic construct; VL-region of MS-Roche#7

<400> 11
 gatatcgtgc tgaccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60
 ctgagctgca gagcgagcca gagcgtgagc agcagctatc tggcgtggta ccagcagaaa 120
 ccaggtcaag caccgcgtct attaatattat ggcgcgagca gccgtgcaac tgggggtcccg 180
 gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240
 cctgaagact ttgcgactta ttattgcttt cagctttatt ctgatacttt tacctttggc 300
 cagggtacga aagttgaaat taaacgtacg 330

<210> 12
 <211> 110
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic construct; VL-region of MS-Roche#7

<400> 12

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu

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65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Leu Tyr Ser Asp Pro
 85 90 95

Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

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<210> 13
<211> 330
<212> DNA
<213> artificial sequence
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<220>
<223> synthetic construct; VL-region of MS-Roche#8
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<400>      13  
gatatcgtgc tgaccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc        60  
  
ctgagctgca gagcgagcca gagcgtgagc agcagctatc tggcgtggta ccagcagaaa       120  
  
ccagggtcaag caccgcgtct attaat ttat ggcgcgagca gccgtgcaac tgggggtccc          180  
  
gcbgcttttta gcbgctcttg atccggcacg gatatttacct tgaccattag cagcctggaa     240  
  
cctgaagaact ttgcgaacta ttattgccag cagctttctt cttttcctcc tacctttggc    300  
  
cagqqtacga aagttagaat taaacgtacg                                     330
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<210> 14
<211> 110
<212> PRT
<213> artificial sequence
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<220>
<223> synthetic construct; VL-region of MS-Roche#8
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<400> 14

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

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Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Ser Ser Phe Pro
 85 90 95

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
 100 105 110

<210> 15
 <211> 24
 <212> DNA
 <213> artificial sequence

<220>
 <223> synthetic construct; CDR3 of VL-region of MS-Roche#3

<400> 15
 cagcaggttt ataatcctcc tggt

24

<210> 16
 <211> 8
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic construct; CDR3 of VL-region of MS-Roche#3

<400> 16

Gln Gln Val Tyr Asn Pro Pro Val
 1 5

<210> 17
 <211> 24
 <212> DNA
 <213> artificial sequence

<220>
 <223> synthetic construct; CDR3 of VL-region of MS-Roche#7

<400> 17
 tttcagcttt attctgatcc tttt

24

<210> 18
 <211> 8
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic construct; CDR3 of VL-region of MS-Roche#7

<400> 18

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Phe Gln Leu Tyr Ser Asp Pro Phe
1 5

<210> 19
<211> 24
<212> DNA
<213> artificial sequence

<220>

<223> synthetic construct; CDR3 of VL-region of MS-Roche#8

<400> 19
cagcagcttt cttcttttcc tcct

24

<210> 20
<211> 8
<212> PRT
<213> artificial sequence

<220>

<223> synthetic construct; CDR3 of VL-region of MS-Roche#8

<400> 20

Gln Gln Leu Ser Ser Phe Pro Pro
1 5

<210> 21
<211> 39
<212> DNA
<213> artificial sequence

<220>

<223> synthetic construct; CDR3 of VH-region of MS-Roche#3

<400> 21
cttactcatt atgctcgta ttatcgttat tttgatgtt

39

<210> 22
<211> 13
<212> PRT
<213> artificial sequence

<220>

<223> synthetic construct; CDR3 of VH-region of MS-Roche#3

<400> 22

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val
1 5 10

<210> 23
<211> 51

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<212> DNA

<213> artificial sequence

<220>

<223> synthetic construct; CDR3 of VH-region of MS-Roche#7

<400> 23

ggtaagggtataactcataa gccttatggt tatgttcgtt attttgatgt t

51

<210> 24

<211> 17

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; CDR3 of VH-region of MS-Roche#7

<400> 24

Gly	Lys	Gly	Asn	Thr	His	Lys	Pro	Tyr	Gly	Tyr	Val	Arg	Tyr	Phe	Asp
1				5					10					15	

Val

<210> 25

<211> 45

<212> DNA

<213> artificial sequence

<220>

<223> synthetic construct; CDR3 of VH-region of MS-Roche#8

<400> 25

cttctttctc gtggttataa tggttattat cataagtttg atggt

45

<210> 26

<211> 15

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; CDR3 of VH-region of MS-Roche#8

<400> 26

Leu	Leu	Ser	Arg	Gly	Tyr	Asn	Gly	Tyr	Tyr	His	Lys	Phe	Asp	Val
1				5				10					15	

<210> 27

<211> 42

<212> PRT

<213> artificial sequence

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<220>

<223> synthetic construct; beta-A4 peptide

<400> 27

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
1 5 10 15

Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
20 25 30

Gly Leu Met Val Gly Gly Val Val Ile Ala
35 40

<210> 28

<211> 17

<212> DNA

<213> artificial sequence

<220>

<223> synthetic construct; VL-primer for

<400> 28

gtggtggttc cgatatc

17

<210> 29

<211> 43

<212> DNA

<213> artificial sequence

<220>

<223> synthetic construct; VL-primer back

<400> 29

agcgtcacac tcggtgcggc ttctggctgg ccaagaacgg tta

43

<210> 30

<211> 17

<212> DNA

<213> artificial sequence

<220>

<223> synthetic construct; control primer for

<400> 30

caggaaacag ctatgac

17

<210> 31

<211> 19

<212> DNA

<213> artificial sequence

<220>

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<223> synthetic construct; control primer back

<400> 31

taccgttgct cttcacccc

19

<210> 32

<211> 360

<212> DNA

<213> artificial sequence

<220>

<223> synthetic construct; VH MS-Roche#3.6H5 x 3.6L2

<400> 32

caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgcg tctgagctgc 60

gcggcctccg gatttacctt tagcagctat gcgatgagct gggcgcgcca agcccctggg 120

aagggctctcg agtgggtgag cgctatttct gagtctggta agactaagta ttatgctgat 180

tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240

atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtct tactcattat 300

gctcgttatt atcgttattt tgatgtttgg ggccaaggca ccctggtgac ggtagctca 360

<210> 33

<211> 120

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; VH MS-Roche#3.6H5 x 3.6L2

<400> 33

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
1 5 10 15Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
20 25 30Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala
35 40 45Ile Ser Glu Ser Gly Lys Thr Lys Tyr Tyr Ala Asp Ser Val Lys Gly
50 55 60Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65 70 75 80

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg

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85

90

95

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 34
 <211> 360
 <212> DNA
 <213> artificial sequence

<220>
 <223> synthetic construct; VH MS-Roche#3.6H8 x 3.6L2

<400> 34
 caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgcg tctgagctgc 60
 gcggcctccg gatttacctt tagcagctat gcgatgagct gggcgcgcca agcccctggg 120
 aagggctctcg agtgggtgag cgctatttct gagtattcta agtttaagta ttatgctgat 180
 tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240
 atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtct tactcattat 300
 gctcgttatt atcggttattt tgatgtttgg ggccaaggca ccctggtgac ggtagctca 360

<210> 35
 <211> 120
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic construct; VH MS-Roche#3.6H8 x 3.6L2

<400> 35

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
 1 5 10 15

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
 20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala
 35 40 45

Ile Ser Glu Tyr Ser Lys Phe Lys Tyr Tyr Ala Asp Ser Val Lys Gly
 50 55 60

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Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65 70 75 80

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
85 90 95

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 36
<211> 372
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; VH MS-Roche#7.4H2 x 7.2L1

<400> 36
caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgcg tctgagctgc 60
gcggcctccg gatttacott tagcagctat gcgatgagct gggcgcgcca agcccctggg 120
aagggtctcg agtgggtgag cgctattaat tataatggtg ctcgtattta ttatgctgat 180
tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240
atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtgg taagggtaat 300
actcataagc cttatggtta tggtcgttat tttgatgttt ggggcccaagg caccctggtg 360
acggttagct ca 372

<210> 37
<211> 124
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VH MS-Roche#7.4H2 x 7.2L1

<400> 37

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
1 5 10 15

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala

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35

40

45

Ile Asn Tyr Asn Gly Ala Arg Ile Tyr Tyr Ala Asp Ser Val Lys Gly
 50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
 65 70 75 80

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
 85 90 95

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
 100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 38
 <211> 372
 <212> DNA
 <213> artificial sequence

<220>
 <223> synthetic construct; VH MS-Roche#7.9H2 x 7.12L2

<400> 38
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 gcggcctcgg gatttacctt tagcagctat gcgatgagct ggggtgcgcca agcccctggg 120
 aaggggtctcg agtgggtgag cgctattaat gctgatggta atcgtaagta ttatgctgat 180
 tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240
 atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtgg taagggtaat 300
 actcataagc cttatgggta tgttcggtat tttgatgttt ggggccaagg caccctggtg 360
 acggttagct ca 372

<210> 39
 <211> 124
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic construct; VH MS-Roche#7.9H2 x 7.12L2

<400> 39

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
 1 5 10 15

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Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
 20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala
 35 40 45

Ile Asn Ala Asp Gly Asn Arg Lys Tyr Tyr Ala Asp Ser Val Lys Gly
 50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
 65 70 75 80

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
 85 90 95

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
 100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 40

<211> 372

<212> DNA

<213> artificial sequence

<220>

<223> synthetic construct; VH MS-Roche#7.9H4 x 7.12L2

<400> 40

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 gcggcctccg gatttacctt tagcagctat gcgatgagct ggggtgcgcca agcccctggg 120
 aagggctctcg agtgggtgag cgctattaat gctgttggtg tgaagaagtt ttatgctgat 180
 tctgttaagg gtcggttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240
 atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtgg taagggtaat 300
 actcataagc cttatgggta tggttcgttat ttgatgttt ggggcccaagg caccctggtg 360
 acggttagct ca 372

<210> 41

<211> 124

<212> PRT

<213> artificial sequence

17/165

<220>

<223> synthetic construct; VH MS-Roche#7.9H4 x 7.12L2

<400> 41

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
 1 5 10 15

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
 20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala
 35 40 45

Ile Asn Ala Val Gly Met Lys Lys Phe Tyr Ala Asp Ser Val Lys Gly
 50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
 65 70 75 80

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
 85 90 95

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
 100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 42

<211> 372

<212> DNA

<213> artificial sequence

<220>

<223> synthetic construct; VH MS-Roche#7.11H1 x 7.11L1

<400> 42

caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgcg tctgagctgc 60
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 aagggtctcg agtgggtgag cggtattaat gctgctggtt ttcgtactta ttatgctgat 180
 tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240
 atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtgg taagggtaat 300
 actcataagc cttatgggta tgttcggttat tttgatgttt ggggccaagg caccctgggtg 360
 acggttagct ca 372

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<210> 43
 <211> 124
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic construct; VH MS-Roche#7.11H1 x 7.11L1

<400> 43

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
 1 5 10 15

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
 20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly
 35 40 45

Ile Asn Ala Ala Gly Phe Arg Thr Tyr Tyr Ala Asp Ser Val Lys Gly
 50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
 65 70 75 80

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
 85 90 95

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
 100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 44
 <211> 372
 <212> DNA
 <213> artificial sequence

<220>
 <223> synthetic construct; VH MS-Roche#7.11H1 x 7.2L1

<400> 44
 caattggtgg aaagcggcgg cggcctggtg caaccggggcg gcagcctgcg tctgagctgc 60
 gcggcctccg gatttacctt tagcagctat gcgatgagct gggcgcgcca agcccctggg 120
 aagggtctcg agtgggtgag cggtattaat gctgctgggt ttcgtactta ttatgctgat 180

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tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240
 atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtgg taagggtaat 300
 actcataagc cttatgggta tgttcgttat tttgatgttt ggggccaagg caccctgggtg 360
 acggttagct ca 372

<210> 45
 <211> 124
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic construct; VH MS-Roche#7.11H1 x 7.2L1

<400> 45

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
 1 5 10 15

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
 20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly
 35 40 45

Ile Asn Ala Ala Gly Phe Arg Thr Tyr Tyr Ala Asp Ser Val Lys Gly
 50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
 65 70 75 80

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
 85 90 95

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
 100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 46
 <211> 330
 <212> DNA
 <213> artificial sequence

<220>
 <223> synthetic construct; VL MS-Roche#3.6H5 x 3.6L2

20/165

```

<400> 46
gatatcgtgc tgaccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc      60
ctgagctgca gagcgagcca gtttctttct cgttattatc tggcgtggta ccagcagaaa      120
ccaggtcaag caccgctctt attaatttat ggcgcgagca gccgtgcaac tgggggtcccg      180
gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa      240
cctgaagact ttgcggttta ttattgccag cagacttata attatcctcc tacctttggc      300
cagggtagca aagttgaaat taaacgtacg                                     330

```

```

<210> 47
<211> 110
<212> PRT
<213> artificial sequence

```

```

<220>
<223> synthetic construct; VL MS-Roche#3.6H5 x 3.6L2

```

```

<400> 47

```

```

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1           5           10           15

```

```

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Phe Leu Ser Arg Tyr
20           25           30

```

```

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35           40           45

```

```

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50           55           60

```

```

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65           70           75           80

```

```

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Thr Tyr Asn Tyr Pro
85           90           95

```

```

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100          105          110

```

```

<210> 48
<211> 330
<212> DNA
<213> artificial sequence

```

```

<220>
<223> synthetic construct; VL MS-Roche#3.6H8 x 3.6L2

```

21/165

<400> 48
 gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcca acgtgcgacc 60
 ctgagctgca gagcgagcca gtttctttct cgttattatc tggcgtggta ccagcagaaa 120
 ccagggtcaag caccgogtct attaatattat ggcgcgagca gccgtgcaac tgggggtcccg 180
 gcgcgttttta ggggctcttg atccggcacg gattttaccc tgaccattag cagcctggaa 240
 cctgaagact ttgcggttta ttattgccag cagacttata attatcctcc tacctttggc 300
 cagggtacga aagttgaaat taaacgtacg 330

<210> 49
 <211> 110
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic construct; VL MS-Roche#3.6H8 x 3.6L2

<400> 49
 Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Phe Leu Ser Arg Tyr
 20 25 30
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45
 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
 50 55 60
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
 65 70 75 80
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Thr Tyr Asn Tyr Pro
 85 90 95
 Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
 100 105 110

<210> 50
 <211> 330
 <212> DNA
 <213> artificial sequence

<220>

22/165

<223> synthetic construct; VL MS-Roche#7.4H2 x 7.2L1

```

<400> 50
gatatcgtgc tgaccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc      60
ctgagctgca gagcgagcca gtatgttgat cgtacttatac tggcgtggta ccagcagaaa      120
ccaggtcaag caccgcgtct attaatattat ggcgcgagca gccgtgcaac tgggggtcccg      180
gcgcggtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa      240
cctgaagact ttgcgactta ttattgccag cagatttatt cttttcctca tacctttggc      300
cagggtagca aagttgaaat taaacgtacg                                     330

```

<210> 51

<211> 110

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; VL MS-Roche#7.4H2 x 7.2L1

<400> 51

```

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1           5           10           15

```

```

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Tyr Val Asp Arg Thr
20           25           30

```

```

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35           40           45

```

```

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50           55           60

```

```

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65           70           75           80

```

```

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ile Tyr Ser Phe Pro
85           90           95

```

```

His Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100          105          110

```

<210> 52

<211> 330

<212> DNA

<213> artificial sequence

23/165

<220>

<223> synthetic construct; VL MS-Roche#7.9H2 x 7.12L2

<400> 52

```

gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc      60
ctgagctgca gagcgagcca gcgttttttt tataagtatc tggcgtggta ccagcagaaa      120
ccagggtcaag caccgcgtct attaatttct ggtttcttcta accgtgcaac tgggggtcccg      180
gcgcgttttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa      240
cctgaagact ttgcggttta ttattgcctt cagctttata atattcctaa tacctttggc      300
cagggtacga aagttgaaat taaacgtacg                                     330

```

<210> 53

<211> 110

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; VL MS-Roche#7.9H2 x 7.12L2

<400> 53

```

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1           5           10           15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Phe Phe Tyr Lys
          20           25           30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
          35           40           45

Ile Ser Gly Ser Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
          50           55           60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65           70           75           80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln Leu Tyr Asn Ile Pro
          85           90           95

Asn Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
          100          105          110

```

<210> 54

<211> 330

<212> DNA

<213> artificial sequence

24/165

<220>

<223> synthetic construct; VL MS-Roche#7.9H4 x 7.12L2

<400> 54

```

gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc      60
ctgagctgca gagcgagcca gcgttttttt tataagtatc tggcgtggta ccagcagaaa      120
ccagggtcaag caccgcgtct attaatcttct gggtcttcta accgtgcaac tgggggtcccg      180
gcgcgttttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa      240
cctgaagact ttgcggttta ttattgcctt cagctttata atattcctaa tacctttggc      300
caggggtacga aagttgaaat taaacgtacg                                     330

```

<210> 55

<211> 110

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; VL MS-Roche#7.9H4 x 7.12L2

<400> 55

```

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1           5           10           15

```

```

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Phe Phe Tyr Lys
          20           25           30

```

```

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
          35           40           45

```

```

Ile Ser Gly Ser Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
          50           55           60

```

```

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65           70           75           80

```

```

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln Leu Tyr Asn Ile Pro
          85           90           95

```

```

Asn Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
          100          105          110

```

<210> 56

<211> 330

<212> DNA

25/165

<213> artificial sequence

<220>

<223> synthetic construct; VL MS-Roche#7.11H1 x 7.11L1

<400> 56

```

gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc      60
ctgagctgca gagcgagcca gcgtattctt cgtattttatc tggcgtggta ccagcagaaa      120
ccagggtcaag caccgcgtct attaatattat ggcgcgagca gccgtgcaac tgggggtccc      180
gcgcgttttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa      240
cctgaagact ttgcgactta ttattgccag cagggtttatt ctctctctca tacctttggc      300
cagggtacga aagttgaaat taaacgtacg                                     330

```

<210> 57

<211> 110

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; VL MS-Roche#7.11H1 x 7.11L1

<400> 57

```

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1           5           10           15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Ile Leu Arg Ile
          20           25           30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
          35           40           45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
          50           55           60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65           70           75           80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Val Tyr Ser Pro Pro
          85           90           95

His Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
          100          105          110

```

<210> 58

<211> 330

26/165

<212> DNA

<213> artificial sequence

<220>

<223> synthetic construct; VL MS-Roche#7.11H1 x 7.2L1

<400> 58

gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcca acgtgcgacc	60
ctgagctgca gagcgagcca gtatgttgat cgtacttata tggcgtggta ccagcagaaa	120
ccaggtaag caccgcgtct attaatattat ggcgcgagca gccgtgcaac tgggggtccc	180
gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa	240
cctgaagact ttgcgactta ttattgccag cagatttatt cttttcctca tacctttggc	300
cagggtagca aagttgaaat taaacgtacg	330

<210> 59

<211> 110

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; VL MS-Roche#7.11H1 x 7.2L1

<400> 59

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly	
1 5 10 15	

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Tyr Val Asp Arg Thr	
20 25 30	

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu	
35 40 45	

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser	
50 55 60	

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu	
65 70 75 80	

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ile Tyr Ser Phe Pro	
85 90 95	

His Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr	
100 105 110	

<210> 60

27/165

<211> 39
<212> DNA
<213> artificial sequence

<220>

<223> HCDR3 MS-Roche#3.6H5 x 3.6L2

<400> 60

cttactcatt atgctcggtta ttatcggtat tttgatggt

39

<210> 61
<211> 13
<212> PRT
<213> artificial sequence

<220>

<223> HCDR3 MS-Roche#3.6H5 x 3.6L2

<400> 61

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val
1 5 10

<210> 62
<211> 39
<212> DNA
<213> artificial sequence

<220>

<223> HCDR3 MS-Roche#3.6H8 x 3.6L2

<400> 62

cttactcatt atgctcggtta ttatcggtat tttgatggt

39

<210> 63
<211> 13
<212> PRT
<213> artificial sequence

<220>

<223> HCDR3 MS-Roche#3.6H8 x 3.6L2

<400> 63

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val
1 5 10

<210> 64
<211> 51
<212> DNA
<213> artificial sequence

<220>

<223> HCDR3 MS-Roche#7.4H2x7.2L1

28/165

<400> 64
ggtaagggtataactcataa gccttatggt tatgttcggt attttgatgt t

51

<210> 65
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> HCDR3 MS-Roche#7.4H2x7.2L1

<400> 65

Gly	Lys	Gly	Asn	Thr	His	Lys	Pro	Tyr	Gly	Tyr	Val	Arg	Tyr	Phe	Asp
1				5					10					15	

Val

<210> 66
<211> 51
<212> DNA
<213> artificial sequence

<220>
<223> HCDR3 MS-Roche#7.9H2x7.12L2

<400> 66
ggtaagggtataactcataa gccttatggt tatgttcggt attttgatgt t

51

<210> 67
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> HCDR3 MS-Roche#7.9H2x7.12L2

<400> 67

Gly	Lys	Gly	Asn	Thr	His	Lys	Pro	Tyr	Gly	Tyr	Val	Arg	Tyr	Phe	Asp
1				5					10					15	

Val

<210> 68
<211> 51
<212> DNA
<213> artificial sequence

<220>
<223> HCDR3 MS-Roche#7.9H4x7.12L2

29/165

<400> 68
ggtaagggtataactcataa gccttatggt tatgttcggt attttgatgt t 51

<210> 69
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> HCDR3 MS-Roche#7.9H4x7.12L2

<400> 69

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
1 5 10 15

Val

<210> 70
<211> 51
<212> DNA
<213> artificial sequence

<220>
<223> HCDR3 MS-Roche#7.11H1x7.11L1

<400> 70
ggtaagggtataactcataa gccttatggt tatgttcggt attttgatgt t 51

<210> 71
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> HCDR3 MS-Roche#7.11H1x7.11L1

<400> 71

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
1 5 10 15

Val

<210> 72
<211> 51
<212> DNA
<213> artificial sequence

<220>

30/165

<223> HCDR3 MS-Roche#7.11H1x7.2L1

<400> 72

ggtaagggtataactcataa gccttatggt tatgttcggt attttgatgt t

51

<210> 73

<211> 17

<212> PRT

<213> artificial sequence

<220>

<223> HCDR3 MS-Roche#7.11H1x7.2L1

<400> 73

Gly	Lys	Gly	Asn	Thr	His	Lys	Pro	Tyr	Gly	Tyr	Val	Arg	Tyr	Phe	Asp
1				5					10					15	

Val

<210> 74

<211> 24

<212> DNA

<213> artificial sequence

<220>

<223> LCDR3 MS-Roche#3.6H5 x 3.6L2

<400> 74

cagcagactt ataattatcc tcct

24

<210> 75

<211> 8

<212> PRT

<213> artificial sequence

<220>

<223> LCDR3 MS-Roche#3.6H5 x 3.6L2

<400> 75

Gln	Gln	Thr	Tyr	Asn	Tyr	Pro	Pro
1				5			

<210> 76

<211> 24

<212> DNA

<213> artificial sequence

<220>

<223> LCDR3 MS-Roche#3.6H8 x 3.6L2

<400> 76

31/165

cagcagactt ataattatcc tcct

24

<210> 77

<211> 8

<212> PRT

<213> artificial sequence

<220>

<223> LCDR3 MS-Roche#3.6H8 x 3.6L2

<400> 77

Gln Gln Thr Tyr Asn Tyr Pro Pro
1 5

<210> 78

<211> 24

<212> DNA

<213> artificial sequence

<220>

<223> LCDR3 MS-Roche#7.4H2x7.2L1

<400> 78

cagcagattt attcttttcc tcat

24

<210> 79

<211> 8

<212> PRT

<213> artificial sequence

<220>

<223> LCDR3 MS-Roche#7.4H2x7.2L1

<400> 79

Gln Gln Ile Tyr Ser Phe Pro His
1 5

<210> 80

<211> 24

<212> DNA

<213> artificial sequence

<220>

<223> LCDR3 MS-Roche#7.9H2x7.12L2

<400> 80

cttcagcttt ataattatcc taat

24

<210> 81

<211> 8

<212> PRT

<213> artificial sequence

32/165

<220>

<223> LCDR3 MS-Roche#7.9H2x7.12L2

<400> 81

Leu Gln Leu Tyr Asn Ile Pro Asn
1 5

<210> 82

<211> 24

<212> DNA

<213> artificial sequence

<220>

<223> LCDR3 MS-Roche#7.9H4x7.12L2

<400> 82

cttcagcttt ataatattcc taat

24

<210> 83

<211> 8

<212> PRT

<213> artificial sequence

<220>

<223> LCDR3 MS-Roche#7.9H4x7.12L2

<400> 83

Leu Gln Leu Tyr Asn Ile Pro Asn
1 5

<210> 84

<211> 24

<212> DNA

<213> artificial sequence

<220>

<223> LCDR3 MS-Roche#7.11H1x7.11L1

<400> 84

cagcagggttt attctcctcc tcat

24

<210> 85

<211> 8

<212> PRT

<213> artificial sequence

<220>

<223> LCDR3 MS-Roche#7.11H1x7.11L1

<400> 85

Gln Gln Val Tyr Ser Pro Pro His

33/165

1

5

<210> 86
<211> 24
<212> DNA
<213> artificial sequence

<220>
<223> LCDR3 MS-Roche#7.11H1x7.2L1

<400> 86
cagcagattt attctttttcc tcat

24

<210> 87
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> LCDR3 MS-Roche#7.11H1x7.2L1

<400> 87

Gln Gln Ile Tyr Ser Phe Pro His
1 5

<210> 88
<211> 378
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; VH MS-Roche#7.9H7

<400> 88
caggtgcaat tgggtgaaag cggcgggcggc ctggtgcaac cgggcggcag cctgcgtctg 60
agctgcgcgg cctccggatt taccttttagc agctatgcga tgagctgggt ggcgaagcc 120
cctgggaagg gtctcgagtg ggtgagcgct attaatgctt ctggtactcg tacttattat 180
gctgattctg ttaagggctg ttttaccatt tcacgtgata attcgaaaaa caccctgtat 240
ctgcaaataga acagcctgcg tgcggaagat acggccgtgt attattgcgc gcgtggtaag 300
ggtaataactc ataagcctta tggttatgtt cgttattttg atgtttgggg ccaaggcacc 360
ctggtgacgg ttagctca 378

<210> 89
<211> 126
<212> PRT
<213> artificial sequence

<220>

34/165

<223> synthetic construct; VH MS-Roche#7.9H7

<400> 89

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Asn Ala Ser Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr
 100 105 110

Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 90

<211> 330

<212> DNA

<213> artificial sequence

<220>

<223> synthetic construct; VL MS-Roche#7.9H7

<400> 90

gatatacgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcca acgtgcgacc 60
 ctgagctgca gagcgagcca gagcgtgagc agcagctatc tggcgtggta ccagcagaaa 120
 ccagggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tgggggtcccg 180
 gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240
 cctgaagact ttgcgactta ttattgcctt cagatttata atatgcctat tacctttggc 300
 cagggtacga aagttgaaat taaacgtacg 330

<210> 91

35/165

<211> 110
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic construct; VL MS-Roche#7.9H7

<400> 91

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Ile Tyr Asn Met Pro
 85 90 95

Ile Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
 100 105 110

<210> 92
 <211> 51
 <212> DNA
 <213> artificial sequence

<220>
 <223> synthetic construct; HCDR3 MS-Roche#7.9H7

<400> 92
 ggtaagggta atactcataa gccttatggg tatgttcggt attttgatgt t

51

<210> 93
 <211> 17
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic construct; HCDR3 MS-Roche#7.9H7

<400> 93

36/165

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
1 5 10 15

Val

<210> 94
<211> 24
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 MS-Roche#7.9H7

<400> 94
cttcagattt ataatatgcc tatt

24

<210> 95
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 MS-Roche#7.9H7

<400> 95

Leu Gln Ile Tyr Asn Met Pro Ile
1 5

<210> 96
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#3

<400> 96

Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala
1 5 10

<210> 97
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR2 of MS-Roche#3

<400> 97

Gly Ala Ser Ser Arg Ala Thr

37/165

1

5

<210> 98
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#3

<400> 98

Gln Gln Val Tyr Asn Pro Pro Val
1 5

<210> 99
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR1 of MS-Roche#3

<400> 99

Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser
1 5 10

<210> 100
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3

<400> 100

Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 101
<211> 13
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR3 of MS-Roche#3

<400> 101

38/165

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val
1 5 10

<210> 102
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#3.1

<400> 102

Gln Gln Val Tyr Ser Val Pro Pro
1 5

<210> 103
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#3.2

<400> 103

Gln Gln Ile Tyr Ser Tyr Pro Pro
1 5

<210> 104
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#3.3

<400> 104

His Gln Met Ser Ser Tyr Pro Pro
1 5

<210> 105
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#3.4

<400> 105

Gln Gln Thr Tyr Asp Tyr Pro Pro
1 5

39/165

<210> 106
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#3.5

<400> 106

Gln Gln Ile Tyr Asp Tyr Pro Pro
1 5

<210> 107
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#3.6

<400> 107

Gln Gln Thr Tyr Asn Tyr Pro Pro
1 5

<210> 108
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.2H1

<400> 108

Ala Ile Ser Glu His Gly Leu Asn Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 109
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.2H2

<400> 109

Ala Ile Ser Gln Arg Gly Gln Phe Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

40/165

Gly

<210> 110
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.3H1

<400> 110

Val	Ile	Ser	Glu	Lys	Ser	Arg	Phe	Ile	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 111
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.3H2

<400> 111

Val	Ile	Ser	Gln	Glu	Ser	Gln	Tyr	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 112
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.3H3

<400> 112

Ala	Ile	Ser	Gln	Asn	Gly	Phe	His	Ile	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

41/165

<210> 113
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.4H1

<400> 113

Ala	Ile	Ser	Glu	Thr	Ser	Ile	Arg	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5				10						15	

Gly

<210> 114
<211> 16
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.4H2

<400> 114

Val	Ile	Asp	Met	Val	Gly	His	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly
1				5				10						15	

<210> 115
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.4H3

<400> 115

Val	Ile	Ser	Gln	Thr	Gly	Arg	Lys	Ile	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5				10						15	

Gly

<210> 116
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.4H4

42/165

<400> 116

Ala Ile Ser Glu Thr Gly Met His Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 117

<211> 17

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; HCDR2 of MS-Roche#3.4H5

<400> 117

Val Ile Ser Gln Val Gly Ala His Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 118

<211> 17

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; HCDR2 of MS-Roche#3.4H6

<400> 118

Ala Ile Ser Glu Ser Gly Trp Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 119

<211> 17

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; HCDR2 of MS-Roche#3.4H7

<400> 119

Val Ile Ser Glu Thr Gly Lys Asn Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

43/165

Gly

<210> 120
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.4H8

<400> 120

Ala	Ile	Ser	Glu	His	Gly	Arg	Phe	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 121
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.4H9

<400> 121

Ala	Ile	Ser	Glu	Ser	Ser	Lys	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 122
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.4H10

<400> 122

Ala	Ile	Ser	Glu	Ser	Gly	Arg	Gly	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

44/165

<210> 123
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.4H11

<400> 123

Ala	Ile	Ser	Glu	Phe	Gly	Lys	Asn	Ile	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 124
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.4H12

<400> 124

Val	Ile	Ser	Gln	Thr	Gly	Gln	Asn	Ile	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 125
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.4H13

<400> 125

Ala	Ile	Ser	Glu	Gln	Gly	Arg	Asn	Ile	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 126
<211> 17
<212> PRT
<213> artificial sequence

45/165

<220>

<223> synthetic construct; HCDR2 of MS-Roche#3.4H14

<400> 126

Ala	Ile	Ser	Glu	Ser	Gly	Gln	Tyr	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 127

<211> 17

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; HCDR2 of MS-Roche#3.4H16

<400> 127

Ala	Ile	Ser	Glu	Ser	Gly	Val	Asn	Ile	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 128

<211> 17

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; HCDR2 of MS-Roche#3.4H17

<400> 128

Ala	Ile	Ser	Glu	Phe	Gly	Gln	Phe	Ile	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 129

<211> 17

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; HCDR2 of MS-Roche#3.4H18

<400> 129

46/165

Ala Ile Ser Gln Gln Ser Asn Phe Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 130
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#3.4L7

<400> 130

Arg Ala Ser Gln Arg Leu Gly Arg Leu Tyr Leu Ala
1 5 10

<210> 131
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#3.4L8

<400> 131

Arg Ala Ser Gln Trp Ile Thr Lys Ser Tyr Leu Ala
1 5 10

<210> 132
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#3.4L9

<400> 132

Arg Ala Ser Arg Arg Ile His Val Tyr Tyr Leu Ala
1 5 10

<210> 133
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#3.4L11

<400> 133

47/165

Arg Ala Ser Gln Leu Val Gly Arg Ala Tyr Leu Ala
1 5 10

<210> 134
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.6H1

<400> 134

Val Ile Ser Glu Ser Gly Gln Tyr Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 135
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.6H2

<400> 135

Val Ile Ser Glu Arg Gly Ile Asn Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 136
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.6H3

<400> 136

Val Ile Ser Glu Thr Gly Lys Phe Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

48/165

<210> 137
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.6H4

<400> 137

Ala	Ile	Ser	Glu	Arg	Gly	Arg	His	Ile	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 138
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.6H5

<400> 138

Ala	Ile	Ser	Glu	Ser	Gly	Lys	Thr	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 139
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.6H6

<400> 139

Ala	Ile	Ser	Glu	His	Gly	Thr	Asn	Ile	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 140
<211> 17
<212> PRT
<213> artificial sequence

49/165

<220>

<223> synthetic construct; HCDR2 of MS-Roche#3.6H8

<400> 140

Ala	Ile	Ser	Glu	Tyr	Ser	Lys	Phe	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 141

<211> 12

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; LCDR1 of MS-Roche#3.6L1

<400> 141

Arg	Ala	Ser	Gln	Phe	Ile	Gln	Arg	Phe	Tyr	Leu	Ala
1				5					10		

<210> 142

<211> 12

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; LCDR1 of MS-Roche#3.6L2

<400> 142

Arg	Ala	Ser	Gln	Phe	Leu	Ser	Arg	Tyr	Tyr	Leu	Ala
1				5					10		

<210> 143

<211> 12

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; LCDR1 of MS-Roche#7

<400> 143

Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ser	Tyr	Leu	Ala
1				5					10		

<210> 144

<211> 7

<212> PRT

<213> artificial sequence

50/165

<220>

<223> synthetic construct; LCDR2 of MS-Roche#7

<400> 144

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 145

<211> 8

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; LCDR3 of MS-Roche#7

<400> 145

Phe Gln Leu Tyr Ser Asp Pro Phe
1 5

<210> 146

<211> 10

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; HCDR1 of MS-Roche#7

<400> 146

Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser
1 5 10

<210> 147

<211> 17

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; HCDR2 of MS-Roche#7

<400> 147

Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 148

<211> 17

<212> PRT

51/165

<213> artificial sequence

<220>

<223> synthetic construct; HCDR3 of MS-Roche#7

<400> 148

Gly	Lys	Gly	Asn	Thr	His	Lys	Pro	Tyr	Gly	Tyr	Val	Arg	Tyr	Phe	Asp
1				5				10						15	

Val

<210> 149

<211> 8

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; LCDR3 of MS-Roche#7.1

<400> 149

His	Gln	Leu	Tyr	Ser	Ser	Pro	Tyr
1				5			

<210> 150

<211> 8

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; LCDR3 of MS-Roche#7.2

<400> 150

Gln	Gln	Ile	Tyr	Ser	Phe	Pro	His
1				5			

<210> 151

<211> 8

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; LCDR3 of MS-Roche#7.3

<400> 151

His	Gln	Val	Tyr	Ser	His	Pro	Phe
1				5			

<210> 152

<211> 8

52/165

<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#7.4

<400> 152

Gln Gln Ile Tyr Asn Phe Pro His
1 5

<210> 153
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#7.5

<400> 153

His Gln Val Tyr Ser Ser Pro Phe
1 5

<210> 154
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#7.6

<400> 154

His Gln Leu Tyr Ser Pro Pro Tyr
1 5

<210> 155
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#7.7

<400> 155

His Gln Val Tyr Ser Ala Pro Phe
1 5

<210> 156
<211> 8
<212> PRT
<213> artificial sequence

53/165

<220>

<223> synthetic construct; LCDR3 of MS-Roche#7.8

<400> 156

His Gln Val Tyr Ser Phe Pro Ile
1 5

<210> 157

<211> 8

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; LCDR3 of MS-Roche#7.9

<400> 157

Leu Gln Ile Tyr Asn Met Pro Ile
1 5

<210> 158

<211> 8

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; LCDR3 of MS-Roche#7.10

<400> 158

Gln Gln Val Tyr Asn Pro Pro His
1 5

<210> 159

<211> 8

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; LCDR3 of MS-Roche#7.11

<400> 159

Gln Gln Val Tyr Ser Pro Pro His
1 5

<210> 160

<211> 12

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; LCDR1 of MS-Roche#7.12

54/165

<400> 160

Arg Ala Ser Gln Tyr Val Ser Ser Pro Tyr Leu Ala
1 5 10

<210> 161

<211> 7

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; LCDR2 of MS-Roche#7.12

<400> 161

Gly Ser Ser Asn Arg Ala Thr
1 5

<210> 162

<211> 8

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; LCDR3 of MS-Roche#7.12

<400> 162

Leu Gln Leu Tyr Asn Ile Pro Asn
1 5

<210> 163

<211> 10

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; HCDR1 of MS-Roche#7.12

<400> 163

Gly Phe Thr Phe Ser Ser Tyr Gly Met Ser
1 5 10

<210> 164

<211> 17

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; HCDR2 of MS-Roche#7.12

<400> 164

Asn Ile Ser Gly Ser Gly Ser Ser Thr Tyr Tyr Ala Asp Ser Val Lys

55/165

1 5 10 15

Gly

<210> 165
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR3 of MS-Roche#7.12

<400> 165

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
1 5 10 15

Val

<210> 166
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#7.13

<400> 166

His Gln Val Tyr Ser Pro Pro Phe
1 5

<210> 167
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.2H1

<400> 167

Ala Ile Asn Ala Asn Gly Leu Lys Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 168
<211> 17

56/165

<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.2H2

<400> 168

Ala	Ile	Asn	Gly	Thr	Gly	Met	Lys	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 169
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.2H3

<400> 169

Ala	Ile	Asn	Ala	Asn	Gly	Tyr	Lys	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 170
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.2H4

<400> 170

Ala	Ile	Asn	Ser	Lys	Gly	Ser	Arg	Ile	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 171
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.2H5

57/165

<400> 171

Ala Ile Asn Ala Thr Gly Arg Ser Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 172

<211> 17

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; HCDR2 of MS-Roche#7.2H6

<400> 172

Ala Ile Asn Ala Arg Gly Asn Arg Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 173

<211> 17

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; HCDR2 of MS-Roche#7.2H7

<400> 173

Ala Ile Asn Ser Arg Gly Ser Asp Thr His Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 174

<211> 17

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; HCDR2 of MS-Roche#7.2H8

<400> 174

Ala Ile Asn Ala Ser Gly His Lys Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

58/165

Gly

<210> 175
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#7.2L1

<400> 175

Arg Ala Ser Gln Tyr Val Asp Arg Thr Tyr Leu Ala
1 5 10

<210> 176
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#7.2L2

<400> 176

Arg Ala Ser Gln Tyr Ile Ser Phe Arg Tyr Leu Ala
1 5 10

<210> 177
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#7.2L4

<400> 177

Arg Ala Ser Gln Phe Ile Arg Arg Ser Tyr Leu Ala
1 5 10

<210> 178
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#7.3H1

<400> 178

His Gln Val Tyr Ser His Pro Phe

59/165

1

5

<210> 179

<211> 17

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; HCDR2 of MS-Roche#7.3H1

<400> 179

Ala Ile Ser Ala Ile Ser Asn Lys Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 180

<211> 12

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; LCDR1 of MS-Roche#7.3L1

<400> 180

Arg Ala Ser Gln Tyr Leu His Tyr Gly Tyr Leu Ala
1 5 10

<210> 181

<211> 17

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; HCDR2 of MS-Roche#7.4H1

<400> 181

Ala Ile Asn Ala Thr Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 182

<211> 17

<212> PRT

<213> artificial sequence

<220>

60/165

<223> synthetic construct; HCDR2 of MS-Roche#7.4H2

<400> 182

Ala	Ile	Asn	Tyr	Asn	Gly	Ala	Arg	Ile	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 183

<211> 8

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; LCDR3 of MS-Roche#7.9H1

<400> 183

Leu	Gln	Ile	Tyr	Asn	Met	Pro	Ile
1				5			

<210> 184

<211> 17

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; HCDR2 of MS-Roche#7.9H1

<400> 184

Ala	Ile	Asn	Ala	Asn	Gly	Gln	Arg	Lys	Phe	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 185

<211> 17

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; HCDR2 of MS-Roche#7.9H2

<400> 185

Ala	Ile	Asn	Ala	Asp	Gly	Asn	Arg	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

61/165

<210> 186
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.9H3
<400> 186

Ala	Ile	Asn	Tyr	Gln	Gly	Asn	Arg	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5				10						15	

Gly

<210> 187
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.9H4
<400> 187

Ala	Ile	Asn	Ala	Val	Gly	Met	Lys	Lys	Phe	Tyr	Ala	Asp	Ser	Val	Lys
1				5				10						15	

Gly

<210> 188
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.9H5
<400> 188

Ala	Ile	Asn	His	Ala	Gly	Asn	Lys	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5				10						15	

Gly

<210> 189
<211> 12

62/165

<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#7.9L1

<400> 189

Arg Ala Ser Gln Arg Leu Ser Pro Arg Tyr Leu Ala
1 5 10

<210> 190
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#7.9L2

<400> 190

Arg Ala Ser Gln Tyr Leu His Lys Arg Tyr Leu Ala
1 5 10

<210> 191
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.9H6

<400> 191

Ala Ile Asn Ala Ser Gly Arg Leu Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 192
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.9H7

<400> 192

Ala Ile Asn Ala Ser Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

63/165

<210> 193
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.9H8

<400> 193

Ala	Ile	Asn	Ala	Ser	Gly	Ser	Lys	Ile	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 194
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.9H9

<400> 194

Ala	Ile	Asn	Gly	Lys	Gly	Asn	Lys	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 195
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.11H1

<400> 195

Gly	Ile	Asn	Ala	Ala	Gly	Phe	Arg	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 196
<211> 17

64/165

<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.11H2

<400> 196

Ala	Ile	Asn	Ala	Asn	Gly	Tyr	Lys	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 197
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.11H3

<400> 197

Gly	Ile	Asn	Ala	Asn	Gly	Asn	Arg	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 198
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.11H4

<400> 198

Ala	Ile	Asn	Ala	Asn	Gly	Tyr	Lys	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 199
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.11H5

65/165

<400> 199

Ala Ile Asn Ala His Gly Gln Arg Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 200

<211> 12

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; LCDR1 of MS-Roche#7.11L1

<400> 200

Arg Ala Ser Gln Arg Ile Leu Arg Ile Tyr Leu Ala
1 5 10

<210> 201

<211> 12

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; LCDR1 of MS-Roche#7.12H1

<400> 201

Arg Ala Ser Gln Tyr Val Phe Arg Arg Tyr Leu Ala
1 5 10

<210> 202

<211> 8

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; LCDR3 of MS-Roche#7.12H1

<400> 202

Leu Gln Leu Tyr Asn Ile Pro Asn
1 5

<210> 203

<211> 10

<212> PRT

<213> artificial sequence

<220>

66/165

<223> synthetic construct; HCDR1 of MS-Roche#7.12H1

<400> 203

Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Gly	Met	Ser
1				5				10	

<210> 204

<211> 17

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; HCDR2 of MS-Roche#7.12H1

<400> 204

Asn	Ile	Asn	Gly	Asn	Gly	Asn	Arg	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5				10						15	

Gly

<210> 205

<211> 17

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; HCDR2 of MS-Roche#7.12L1

<400> 205

Asn	Ile	Ser	Gly	Ser	Gly	Ser	Ser	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5				10						15	

Gly

<210> 206

<211> 12

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; LCDR1 of MS-Roche#7.12L2

<400> 206

Arg	Ala	Ser	Gln	Arg	Phe	Phe	Tyr	Lys	Tyr	Leu	Ala
1				5				10			

<210> 207

67/165

<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#7.12L3
<400> 207

Arg Ala Ser Gln Phe Val Arg Arg Gly Phe Leu Ala
1 5 10

<210> 208
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#7.12L4
<400> 208

Arg Ala Ser Gln Arg Leu Lys Arg Ser Tyr Leu Ala
1 5 10

<210> 209
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#7.12L6
<400> 209

Arg Ala Ser Gln Tyr Leu Trp Tyr Arg Tyr Leu Ala
1 5 10

<210> 210
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#7.12L7
<400> 210

Arg Ala Ser Gln Trp Ile Arg Lys Thr Tyr Leu Ala
1 5 10

<210> 211
<211> 12
<212> PRT
<213> artificial sequence

68/165

<220>
<223> synthetic construct; LCDR1 of MS-Roche#8

<400> 211

Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala
1 5 10

<210> 212
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR2 of MS-Roche#8

<400> 212

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 213
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#8

<400> 213

Gln Gln Leu Ser Ser Phe Pro Pro
1 5

<210> 214
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR1 of MS-Roche#8

<400> 214

Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser
1 5 10

<210> 215
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#8

69/165

<400> 215

Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 216

<211> 15

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; HCDR3 of MS-Roche#8

<400> 216

Leu Leu Ser Arg Gly Tyr Asn Gly Tyr Tyr His Lys Phe Asp Val
1 5 10 15

<210> 217

<211> 8

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; LCDR3 of MS-Roche#8.1

<400> 217

Gln Gln Leu Ser Asn Tyr Pro Pro
1 5

<210> 218

<211> 8

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; LCDR3 of MS-Roche#8.2

<400> 218

Gln Gln Leu Ser Ser Tyr Pro Pro
1 5

<210> 219

<211> 17

<212> PRT

<213> artificial sequence

<220>

70/165

<223> synthetic construct; HCDR2 of MS-Roche#8.1H1

<400> 219

Ala	Ile	Ser	Arg	Ser	Gly	Ser	Asn	Ile	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 220

<211> 8

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; LCDR3 of MS-Roche#8.2H1

<400> 220

Gln	Gln	Leu	Ser	Ser	Tyr	Pro	Pro
1				5			

<210> 221

<211> 17

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; HCDR2 of MS-Roche#8.2H1

<400> 221

Ala	Ile	Ser	Ile	Thr	Gly	Arg	Arg	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

<210> 222

<211> 17

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; HCDR2 of MS-Roche#8.2H2

<400> 222

Ala	Ile	Ser	Arg	Thr	Gly	Ser	Lys	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
1				5					10					15	

Gly

71/165

<210> 223
<211> 16
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#8.2H4

<400> 223

Ala Thr Ser Val Lys Gly Lys Thr Tyr Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 224
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#8.2L1

<400> 224

Arg Ala Ser Gln Arg Val Ser Gly Arg Tyr Leu Ala
1 5 10

<210> 225
<211> 109
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VL kappal

<220>
<221> MISC_FEATURE
<222> (96)..(96)
<223> Xaa = any amino acid of a mixture of Ala, Asp, Glu, Phe, Gly, His
, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, or
Tyr

<220>
<221> MISC_FEATURE
<222> (93)..(93)
<223> Xaa = any amino acid of a mixture of Ala, Asp, Gly, His, Leu, Asn
or Ser

<220>
<221> MISC_FEATURE
<222> (92)..(92)
<223> Xaa = any amino acid of a mixture of Asp, Gly, Asn, Ser or Tyr

72/165

<220>

<221> MISC_FEATURE

<222> (91)..(91)

<223> Xaa = any amino acid of a mixture of Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Gln, Arg, Ser, Thr, Val, Trp or Tyr

<220>

<221> MISC_FEATURE

<222> (89)..(89)

<223> Xaa = any amino acid of a mixture of Phe, His, Ile, Leu, Met or Gln,

<220>

<221> MISC_FEATURE

<222> (85)..(85)

<223> Xaa = can be Thr or Val

<220>

<221> MISC_FEATURE

<222> (94)..(94)

<223> Xaa = any amino acid of a mixture of Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, or Tyr

<220>

<221> MISC_FEATURE

<222> (95)..(95)

<223> Xaa = any amino acid of a mixture of Leu, Pro or Ser

<400> 225

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5					10					15	

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Ser	Ser	Tyr
		20						25					30		

Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			

Tyr	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				

Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75				80	

Glu	Asp	Phe	Ala	Xaa	Tyr	Tyr	Cys	Xaa	Gln	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				85					90					95	

73/165

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105

<210> 226
<211> 114
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VL kappa2

<220>
<221> misc_feature
<222> (101)..(101)
<223> Xaa = any amino acid of a mixture of Ala, Asp, Glu, Phe, Gly, His
, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, or
Tyr

<220>
<221> misc_feature
<222> (94)..(94)
<223> Xaa = any amino acid of a mixture of Phe, His, Ile, Leu, Met or G
ln,

<220>
<221> misc_feature
<222> (96)..(96)
<223> Xaa = any amino acid of a mixture of Ala, Asp, Glu, Phe, Gly, His
, Ile, Lys, Leu, Met, Asn, Gln, Arg, Ser, Thr, Val, Trp or Tyr

<220>
<221> misc_feature
<222> (97)..(97)
<223> Xaa = any amino acid of a mixture of Asp, Gly, Asn, Ser or Tyr

<220>
<221> misc_feature
<222> (98)..(98)
<223> Xaa = any amino acid of a mixture of Ala, Asp, Gly, His, Leu, Asn
or Ser

<220>
<221> misc_feature
<222> (99)..(99)
<223> Xaa = any amino acid of a mixture of Ala, Asp, Glu, Phe, Gly, His
, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, or
Tyr

<220>
<221> misc_feature

74/165

<222> (100)..(100)

<223> Xaa = any amino acid of a mixture of Leu, Pro or Ser

<400> 226

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
 1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
 20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
 50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Xaa Gln Xaa
 85 90 95

Xaa Xaa Xaa Xaa Xaa Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105 110

Arg Thr

<210> 227

<211> 110

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; VL kappa3

<220>

<221> misc_feature

<222> (97)..(97)

<223> Xaa = any amino acid of a mixture of Ala, Asp, Glu, Phe, Gly, His
 , Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, or
 Tyr

<220>

<221> misc_feature

<222> (90)..(90)

<223> Xaa = any amino acid of a mixture of Phe, His, Ile, Leu, Met or G
 ln,

75/165

<220>
 <221> misc_feature
 <222> (86)..(86)
 <223> Xaa = Thr or Val

<220>
 <221> misc_feature
 <222> (92)..(92)
 <223> Xaa = any amino acid of a mixture of Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Gln, Arg, Ser, Thr, Val, Trp or Tyr

<220>
 <221> misc_feature
 <222> (93)..(93)
 <223> Xaa = any amino acid of a mixture of Asp, Gly, Asn, Ser or Tyr

<220>
 <221> misc_feature
 <222> (94)..(94)
 <223> Xaa = any amino acid of a mixture of Ala, Asp, Gly, His, Leu, Asn or Ser

<220>
 <221> misc_feature
 <222> (95)..(95)
 <223> Xaa = any amino acid of a mixture of Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, or Tyr

<220>
 <221> misc_feature
 <222> (96)..(96)
 <223> Xaa = any amino acid of a mixture of Leu, Pro or Ser

<400> 227

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
 50 55 60

76/165

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Xaa Tyr Tyr Cys Xaa Gln Xaa Xaa Xaa Xaa Xaa
85 90 95

Xaa Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 228

<211> 115

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; VL kappa4

<220>

<221> MISC_FEATURE

<222> (102)..(102)

<223> Xaa = any amino acid of a mixture of Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, or Tyr

<220>

<221> MISC_FEATURE

<222> (95)..(95)

<223> Xaa = any amino acid of a mixture of Phe, His, Ile, Leu, Met or Gln,

<220>

<221> MISC_FEATURE

<222> (97)..(97)

<223> Xaa = any amino acid of a mixture of Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Gln, Arg, Ser, Thr, Val, Trp or Tyr

<220>

<221> MISC_FEATURE

<222> (98)..(98)

<223> Xaa = any amino acid of a mixture of Asp, Gly, Asn, Ser or Tyr

<220>

<221> MISC_FEATURE

<222> (99)..(99)

<223> Xaa = any amino acid of a mixture of Ala, Asp, Gly, His, Leu, Asn or Ser

<220>

<221> MISC_FEATURE

<222> (100)..(100)

77/165

<223> Xaa = any amino acid of a mixture of Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, or Tyr

<220>

<221> MISC_FEATURE

<222> (101)..(101)

<223> Xaa = any amino acid of a mixture of Leu, Pro or Ser

<400> 228

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Xaa Gln
85 90 95

Xaa Xaa Xaa Xaa Xaa Xaa Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Thr
115

<210> 229

<211> 111

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; VL lambda1

<220>

<221> MISC_FEATURE

<222> (99)..(99)

<223> Xaa = any amino acid

78/165

<220>
<221> MISC_FEATURE
<222> (97)..(98)
<223> Xaa = any amino acid except a Cys or a deletion

<220>
<221> MISC_FEATURE
<222> (94)..(96)
<223> Xaa = any amino acid except a Cys

<220>
<221> MISC_FEATURE
<222> (92)..(92)
<223> Xaa = any amino acid of Cys, Phe, His, Arg, Trp or Tyr

<400> 229

Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Xaa Asp Xaa Xaa Xaa
85 90 95

Xaa Xaa Xaa Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 230
<211> 112
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VL lambda2

<220>
<221> MISC_FEATURE
<222> (100)..(100)

79/165

<223> Xaa = any amino acid

<220>

<221> MISC_FEATURE

<222> (93)..(93)

<223> Xaa = any amino acid of Cys, Phe, His, Arg, Trp or Tyr

<220>

<221> MISC_FEATURE

<222> (95)..(97)

<223> Xaa = any amino acid except a Cys

<220>

<221> MISC_FEATURE

<222> (98)..(99)

<223> Xaa = any amino acid except a Cys or a deletion

<400> 230

Asp	Ile	Ala	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser	Pro	Gly	Gln
1				5					10					15	

Ser	Ile	Thr	Ile	Ser	Cys	Thr	Gly	Thr	Ser	Ser	Asp	Val	Gly	Gly	Tyr
			20					25					30		

Asn	Tyr	Val	Ser	Trp	Tyr	Gln	Gln	His	Pro	Gly	Lys	Ala	Pro	Lys	Leu
		35					40					45			

Met	Ile	Tyr	Asp	Val	Ser	Asn	Arg	Pro	Ser	Gly	Val	Ser	Asn	Arg	Phe
	50					55					60				

Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Ser	Gly	Leu
65					70					75					80

Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Ser	Xaa	Asp	Xaa	Xaa
				85					90					95	

Xaa	Xaa	Xaa	Xaa	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly
			100					105					110		

<210> 231

<211> 109

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; VL lambda3

80/165

<220>
 <221> MISC_FEATURE
 <222> (97)..(97)
 <223> Xaa = any amino acid

<220>
 <221> MISC_FEATURE
 <222> (90)..(90)
 <223> Xaa = any amino acid of Cys, Phe, His, Arg, Trp or Tyr

<220>
 <221> MISC_FEATURE
 <222> (92)..(94)
 <223> Xaa = any amino acid except a Cys

<220>
 <221> MISC_FEATURE
 <222> (95)..(96)
 <223> Xaa = any amino acid except a Cys or a deletion

<400> 231

Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
 1 5 10 15

Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asp Lys Tyr Ala
 20 25 30

Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
 35 40 45

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
 50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
 65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Xaa Asp Xaa Xaa Xaa Xaa Xaa
 85 90 95

Xaa Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
 100 105

<210> 232
 <211> 127
 <212> PRT
 <213> artificial sequence

81/165

<220>

<223> synthetic construct; VH1A

<220>

<221> MISC_FEATURE

<222> (99)..(112)

<223> Xaa = any amino acid or a deletion

<220>

<221> MISC_FEATURE

<222> (116)..(116)

<223> Xaa = any amino acid out of a mixture of Phe, His, Ile, Leu, Asn, Pro, Ser, Val, Trp or Tyr

<220>

<221> MISC_FEATURE

<222> (114)..(114)

<223> Xaa = any amino acid out of a mixture of Ala, Asp, Glu, Phe, Gly, Ile, Leu, Met, Pro, Gln, Ser, Thr, Val or Tyr

<220>

<221> MISC_FEATURE

<222> (113)..(113)

<223> Xaa = any amino acid

<400> 232

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser
1				5					10					15	

Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	Ser	Ser	Tyr
			20					25					30		

Ala	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
		35					40					45			

Gly	Gly	Ile	Ile	Pro	Ile	Phe	Gly	Thr	Ala	Asn	Tyr	Ala	Gln	Lys	Phe
	50					55					60				

Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Glu	Ser	Thr	Ser	Thr	Ala	Tyr
65					70					75					80

Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	

Ala	Arg	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			100					105					110		

82/165

Xaa Xaa Asp Xaa Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 233
 <211> 127
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic construct; VH1B

<220>
 <221> MISC_FEATURE
 <222> (99)..(112)
 <223> Xaa = any amino acid or a deletion

<220>
 <221> MISC_FEATURE
 <222> (113)..(113)
 <223> Xaa = any amino acid

<220>
 <221> MISC_FEATURE
 <222> (114)..(114)
 <223> Xaa = any amino acid out of a mixture of Ala, Asp, Glu, Phe, Gly,
 Ile, Leu, Met, Pro, Gln, Ser, Thr, Val or Tyr

<220>
 <221> MISC_FEATURE
 <222> (116)..(116)
 <223> Xaa = any amino acid out of a mixture of Phe, His, Ile, Leu, Asn,
 Pro, Ser, Val, Trp or Tyr

<400> 233

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80

83/165

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 100 105 110

Xaa Xaa Asp Xaa Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 234

<211> 128

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; VH2

<220>

<221> MISC_FEATURE

<222> (100)..(113)

<223> Xaa = any amino acid or a deletion

<220>

<221> MISC_FEATURE

<222> (114)..(114)

<223> Xaa = any amino acid

<220>

<221> MISC_FEATURE

<222> (117)..(117)

<223> Xaa = any amino acid out of a mixture of Phe, His, Ile, Leu, Asn,
 Pro, Ser, Val, Trp or Tyr

<220>

<221> MISC_FEATURE

<222> (115)..(115)

<223> Xaa = any amino acid out of a mixture of Ala, Asp, Glu, Phe, Gly,
 Ile, Leu, Met, Pro, Gln, Ser, Thr, Val or Tyr

<400> 234

Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
 20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45

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Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
 50 55 60

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
 85 90 95

Cys Ala Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 100 105 110

Xaa Xaa Xaa Asp Xaa Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 235
 <211> 127
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic construct; VH3

<220>
 <221> MISC_FEATURE
 <222> (99)..(112)
 <223> Xaa = any amino acid or a deletion

<220>
 <221> MISC_FEATURE
 <222> (113)..(113)
 <223> Xaa = any amino acid

<220>
 <221> MISC_FEATURE
 <222> (116)..(116)
 <223> Xaa = any amino acid out of a mixture of Phe, His, Ile, Leu, Asn,
 Pro, Ser, Val, Trp or Tyr

<220>
 <221> MISC_FEATURE
 <222> (114)..(114)
 <223> Xaa = any amino acid out of a mixture of Ala, Asp, Glu, Phe, Gly,
 Ile, Leu, Met, Pro, Gln, Ser, Thr, Val or Tyr

<400> 235

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1	5							10					15				
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr		
			20					25					30				
Ala	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val		
		35					40					45					
Ser	Ala	Ile	Ser	Gly	Ser	Gly	Gly	Ser	Thr	Tyr	Tyr	Ala	Asp	Ser	Val		
	50					55					60						
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr		
65					70					75					80		
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys		
				85					90					95			
Ala	Arg	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa		
			100					105					110				
Xaa	Xaa	Asp	Xaa	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser			
		115					120					125					

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<210> 236
<211> 126
<212> PRT
<213> artificial sequence
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<220>
<223> synthetic construct; VH4
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<221> MISC_FEATURE
<222> (98)..(111)
<223> Xaa = any amino acid or a deletion
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<220>
<221> MISC_FEATURE
<222> (112)..(112)
<223> Xaa = any amino acid
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<220>
<221> MISC_FEATURE
<222> (113)..(113)
<223> Xaa = any amino acid out of a mixture of Ala, Asp, Glu, Phe, Gly,
      Ile, Leu, Met, Pro, Gln, Ser, Thr, Val or Tyr

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<220>

86/165

<221> MISC_FEATURE

<222> (115)..(115)

<223> Xaa = any amino acid out of a mixture of Phe, His, Ile, Leu, Asn,
Pro, Ser, Val, Trp or Tyr

<400> 236

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
20 25 30Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110Xaa Asp Xaa Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 237

<211> 127

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; VH5

<220>

<221> MISC_FEATURE

<222> (99)..(112)

<223> Xaa = any amino acid or a deletion

<220>

<221> MISC_FEATURE

<222> (113)..(113)

<223> Xaa = any amino acid

87/165

<220>

<221> MISC_FEATURE

<222> (116)..(116)

<223> Xaa = any amino acid out of a mixture of Phe, His, Ile, Leu, Asn,
Pro, Ser, Val, Trp or Tyr

<220>

<221> MISC_FEATURE

<222> (114)..(114)

<223> Xaa = any amino acid out of a mixture of Ala, Asp, Glu, Phe, Gly,
Ile, Leu, Met, Pro, Gln, Ser, Thr, Val or Tyr

<400> 237

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95Ala Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110Xaa Xaa Asp Xaa Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 238

<211> 130

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct; VH6

<220>

<221> MISC_FEATURE

88/165

<222> (102)..(115)

<223> Xaa = any amino acid or a deletion

<220>

<221> MISC_FEATURE

<222> (116)..(116)

<223> Xaa = any amino acid

<220>

<221> MISC_FEATURE

<222> (119)..(119)

<223> Xaa = any amino acid out of a mixture of Phe, His, Ile, Leu, Asn, Pro, Ser, Val, Trp or Tyr

<220>

<221> MISC_FEATURE

<222> (117)..(117)

<223> Xaa = any amino acid out of a mixture of Ala, Asp, Glu, Phe, Gly, Ile, Leu, Met, Pro, Gln, Ser, Thr, Val or Tyr

<400> 238

Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Gln
1				5					10					15	

Thr	Leu	Ser	Leu	Thr	Cys	Ala	Ile	Ser	Gly	Asp	Ser	Val	Ser	Ser	Asn
			20					25					30		

Ser	Ala	Ala	Trp	Asn	Trp	Ile	Arg	Gln	Ser	Pro	Gly	Arg	Gly	Leu	Glu
		35					40					45			

Trp	Leu	Gly	Arg	Thr	Tyr	Tyr	Arg	Ser	Lys	Trp	Tyr	Asn	Asp	Tyr	Ala
	50					55					60				

Val	Ser	Val	Lys	Ser	Arg	Ile	Thr	Ile	Asn	Pro	Asp	Thr	Ser	Lys	Asn
65					70					75					80

Gln	Phe	Ser	Leu	Gln	Leu	Asn	Ser	Val	Thr	Pro	Glu	Asp	Thr	Ala	Val
				85					90					95	

Tyr	Tyr	Cys	Ala	Arg	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			100				105							110	

Xaa	Xaa	Xaa	Xaa	Xaa	Asp	Xaa	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val
		115						120				125			

Ser Ser

89/165

130

<210> 239
<211> 327
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; VL kappal

<220>
<221> misc_feature
<222> (286)..(288)
<223> nnn = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT,
CAG, CGT, TCT, ACT, GTT, TGG or TAT

<220>
<221> misc_feature
<222> (271)..(273)
<223> nnn = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CAG,
CGT, TCT, ACT, GTT, TGG or TAT

<220>
<221> misc_feature
<222> (265)..(267)
<223> nnn = TTT, CAT, CTT, ATG or CAG

<220>
<221> misc_feature
<222> (253)..(256)
<223> nnn = can be ACT or GTT

<220>
<221> misc_feature
<222> (283)..(285)
<223> nnn = CTT, CCT or TCT

<220>
<221> misc_feature
<222> (280)..(282)
<223> nnn = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT,
CAG, CGT, TCT, ACT, GTT, TGG or TAT

<220>
<221> misc_feature
<222> (277)..(279)
<223> nnn = GCT, GAT, GGT, CAT, CTT, AAT or TCT

<220>
<221> misc_feature
<222> (274)..(276)

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<223> nnn = GAT, GGT, AAT, TCT or TAT

<400> 239
gatatccaga tgacccagag cccgtctagc ctgagcgcga gcgtgggtga tcgtgtgacc 60
attacctgca gagcgagcca gggcattagc agctatctgg cgtgggtacca gcagaaacca 120
ggtaaagcac cgaaactatt aatttatgca gccagcagct tgcaaagcgg ggtcccgtcc 180
cgtttttagcg gctctggatc cggcactgat tttaccctga ccattagcag cctgcaacct 240
gaagactttg cgnnntatta ttgcnnncag nnnnnnnnnn nnnnnnnnac ctttggccag 300
ggtacgaaag ttgaaattaa acgtacg 327

<210> 240

<211> 328

<212> DNA

<213> artificial sequence

<220>

<223> synthetic construct; VL kappa2

<220>

<221> misc_feature

<222> (289)..(289)

<223> n = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT, C
AG, CGT, TCT, ACT, GTT, TGG or TAT

<220>

<221> misc_feature

<222> (280)..(280)

<223> n = TTT, CAT, CTT, ATG or CAG

<220>

<221> misc_feature

<222> (284)..(284)

<223> n = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CAG, C
GT, TCT, ACT, GTT, TGG or TAT

<220>

<221> misc_feature

<222> (285)..(285)

<223> n = GAT, GGT, AAT, TCT or TAT

<220>

<221> misc_feature

<222> (286)..(289)

<223> n = GCT, GAT, GGT, CAT, CTT, AAT or TCT

<220>

<221> misc_feature

91/165

<222> (287)..(287)

<223> n = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT, CAG, CGT, TCT, ACT, GTT, TGG or TAT

<220>

<221> misc_feature

<222> (288)..(288)

<223> n = CTT, CCT or TCT

<400> 240

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gatatcgtga tgaccagag cccactgagc ctgccagtga ctccgggcga gcctgcgagc      60
attagctgca gaagcagcca aagcctgctg catagcaacg gctataacta tctggattgg      120
taccttcaaa aaccaggtca aagcccgag ctattaattt atctgggcag caaccgtgcc      180
agtgggggtcc cggatcgttt tagcggctct ggatccggca ccgattttac cctgaaaatt      240
agccgtgtgg aagctgaaga cgtgggcgtg tattattgcn cagnnnnnna cctttggcca      300
gggtacgaaa gttgaaatta aacgtacg                                     328
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<210> 241

<211> 330

<212> DNA

<213> artificial sequence

<220>

<223> synthetic construct; VL kappa3

<220>

<221> misc_feature

<222> (289)..(291)

<223> nnn = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT, CAG, CGT, TCT, ACT, GTT, TGG or TAT

<220>

<221> misc_feature

<222> (256)..(258)

<223> nnn = can be ACT or GTT

<220>

<221> misc_feature

<222> (265)..(276)

<223> nnn = TTT, CAT, CTT, ATG or CAG

<220>

<221> misc_feature

<222> (274)..(276)

<223> nnn = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CAG, CGT, TCT, ACT, GTT, TGG or TAT

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<220>
<221> misc_feature
<222> (277)..(279)
<223> nnn = GAT, GGT, AAT, TCT or TAT

<220>
<221> misc_feature
<222> (280)..(282)
<223> nnn = GCT, GAT, GGT, CAT, CTT, AAT or TCT

<220>
<221> misc_feature
<222> (283)..(285)
<223> nnn = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT,
CAG, CGT, TCT, ACT, GTT, TGG or TAT

<220>
<221> misc_feature
<222> (286)..(288)
<223> nnn = CTT, CCT or TCT

<400> 241
gatatcgtgc tgaccacagag cccggcgcacc ctgagcctgt ctccgggcga acgtgcgacc 60
ctgagctgca gacgcagcca gagcgtgagc agcagctatc tggcgtggta ccagcagaaa 120
ccaggtcaag caccgcgtct attaatattat ggcgcgagca gccgtgcaac tgggggtcccg 180
gcgcgtttta gcggtctctg atccggcacg gattttaccc tgaccattag cagcctggaa 240
cctgaagact ttgcgnnnta ttattgcnnn cagnnnnnnn nnnnnnnnnn nacctttggc 300
caggggtacga aagttgaaat taaacgtacg 330

<210> 242
<211> 345
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; VL kappa4

<220>
<221> misc_feature
<222> (304)..(306)
<223> nnn = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT,
CAG, CGT, TCT, ACT, GTT, TGG or TAT

<220>
<221> misc_feature
<222> (283)..(285)
<223> nnn = TTT, CAT, CTT, ATG or CAG

93/165

<220>
<221> misc_feature
<222> (289)..(291)
<223> nnn = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CAG,
CGT, TCT, ACT, GTT, TGG or TAT

<220>
<221> misc_feature
<222> (292)..(294)
<223> nnn = GAT, GGT, AAT, TCT or TAT

<220>
<221> misc_feature
<222> (295)..(297)
<223> nnn = GCT, GAT, GGT, CAT, CTT, AAT or TCT

<220>
<221> misc_feature
<222> (298)..(300)
<223> nnn = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT,
CAG, CGT, TCT, ACT, GTT, TGG or TAT

<220>
<221> misc_feature
<222> (301)..(303)
<223> nnn = CTT, CCT or TCT

<400> 242
gatatcgtga tgacccagag cccggatagc ctggcgggtga gcctggggcga acgtgcgacc 60
attaactgca gaagcagcca gagcgtgctg tatagcagca acaacaaaaa ctatctggcg 120
tggtaccagc agaaaccagg tcagccgccg aaactattaa tttattggggc atccacccgt 180
gaaagcgggg tcccggatcg ttttagcggc tctggatccg gcaactgattt taccctgacc 240
atttcgtccc tgcaagctga agacgtggcg gtgtattatt gcnncagnn nnnnnnnnnn 300
nnnnnnacct ttggccaggg tacgaaagtt gaaattaaac gtacg 345

<210> 243
<211> 322
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; VL lambda1

<220>
<221> misc_feature
<222> (274)..(274)
<223> n = TGT, TTT, CAT, CGT, TGG or TAT

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<220>
<221> misc_feature
<222> (278)..(280)
<223> n = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT, C
AG, CGT, TCT, ACT, GTT, TGG or TAT

<220>
<221> misc_feature
<222> (281)..(282)
<223> n = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT, C
AG, CGT, TCT, ACT, GTT, TGG or TAT or a deletion

<220>
<221> misc_feature
<222> (283)..(283)
<223> n = GCT, TGT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, C
CT, CAG, CGT, TCT, ACT, GTT, TGG or TAT

<400> 243
gatatcgtgc tgaccagcc gccttcagt agtggcgcac caggtcagcg tgtgaccatc 60
tcgtgtagcg gcagcagcag caacattggc agcaactatg tgagctggta ccagcagttg 120
cccgggaagg cgccgaaact gctgatttat gataacaacc agcgtccctc aggcgtgccg 180
gacggtttta gcggatccaa aagcggcacc agcgcgagcc ttgcgattac gggcctgcaa 240
agcgaagacg aagcggatta ttattgccag tctngatnnn nnngtgtttg gcggcggcac 300
gaagttaacc gttcttggcc ag 322

<210> 244
<211> 336
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; VL lambda2

<220>
<221> misc_feature
<222> (274)..(276)
<223> nnn = TGT, TTT, CAT, CGT, TGG or TAT

<220>
<221> misc_feature
<222> (290)..(295)
<223> nnn = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT,
CAG, CGT, TCT, ACT, GTT, TGG or TAT or a deletion

<220>

95/165

<221> misc_feature
<222> (296)..(298)
<223> nnn = GCT, TGT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT,
CCT, CAG, CGT, TCT, ACT, GTT, TGG or TAT

<220>
<221> misc_feature
<222> (280)..(289)
<223> nnn = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT,
CAG, CGT, TCT, ACT, GTT, TGG or TAT

<400> 244
gatatcgcac tgaccagcc agcttcagtg agcggtcac caggtcagag cattaccatc 60
tcgtgtacgg gtactagcag cgatgtgggc ggctataact atgtgagctg gtaccagcag 120
catcccggga aggcgccgaa actgatgatt tatgatgtga gcaaccgtcc ctccaggcgtg 180
agcaaccgtt ttagcggatc caaaagcggc aacaccgcga gcctgaccat tagcggcctg 240
caagcggaag acgaagcgga ttattattgc cagnnngatn nnnnnnnnnn nnnnnnngtg 300
tttgcgggcg gcacgaagtt aaccgttctt ggccag 336

<210> 245
<211> 327
<212> DNA
<213> artificial sequence

<220>
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<220>
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<223> nnn = TGT, TTT, CAT, CGT, TGG or TAT

<220>
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CCT, CAG, CGT, TCT, ACT, GTT, TGG or TAT

<220>
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<223> nnn = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT,
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<220>
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CAG, CGT, TCT, ACT, GTT, TGG or TAT

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caggcgccag ttctggtgat ttatgatgat tctgaccgtc cctcaggcat cccggaacgc      180
tttagcggat ccaacagcgg caacaccgcg accctgacca ttagcggcac tcaggcggaa      240
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<223> nnn = GCT, TGT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT, CAG, CGT, TCT, ACT, GTT, TGG or TAT or a deletion

<400> 246

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cctgggcagg gtctcgagtg gatgggcggc attattccga tttttggcac ggcgaactac      180

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gcgcagaagt ttcagggccg ggtgaccatt accgcggatg aaagcaccag caccgcgtat 240
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 <223> nnn = TTT, CAT, ATT, CTT, AAT, CCT, TCT, GTT, TGG or TAT

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 <223> nnn = GCT, TGT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT, CAG, CGT, TCT, ACT, GTT, TGG or TAT or a deletion

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 cctgggcagg gtctcgagt gatgggctgg attaaccoga atagcggcgg cacgaactac 180
 gcgcagaagt ttcagggccg ggtgaccatg acccgtgata ccagcattag caccgcgtat 240
 atggaactga gcagcctgcg tagcgaagat acggccgtgt attattgcgc gcgtnnnnnn 300
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 <212> DNA
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 <223> synthetic construct; VH2

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 <223> nnn = GCT, TGT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT, CAG, CGT, TCT, ACT, GTT, TGG or TAT or a deletion

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 <223> nnn = GCT, TGT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT, CAG, CGT, TCT, ACT, GTT, TGG or TAT

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 <222> (343)..(345)
 <223> nnn = GCT, GAT, GAG, TTT, GGT, ATT, CTT, ATG, CCT, CAG, TCT, ACT, GTT or TAT

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 cagccgcctg ggaaagccct cgagtggctg gctctgattg attgggatga tgataagtat 180
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 gtgctgacta tgaccaacat ggacccgggtg gatacggcca cctattattg cgcgcgtnnn 300
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<210> 249
 <211> 349
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<220>
 <223> synthetic construct; VH3

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<220>
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TT or TAT

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<210> 250
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<222> (306)..(306)

<223> n = GCT, TGT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, C
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<220>

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<222> (307)..(307)

<223> n = GCT, GAT, GAG, TTT, GGT, ATT, CTT, ATG, CCT, CAG, TCT, ACT, G
TT or TAT

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cctgggaagg gtctcgagtg gattggctat atttattata gcggcagcac caactataat 180

ccgagcctga aaagccgggt gaccattagc gttgatactt cgaaaaacca gtttagcctg 240

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<220>

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<223> n = TTT, CAT, ATT, CTT, AAT, CCT, TCT, GTT, TGG or TAT

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<222> (295)..(304)

<223> n = GCT, TGT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, C
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<220>

<221> misc_feature

<222> (308)..(310)

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TT or TAT

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<210> 252

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<222> (346)..(348)

<223> nnn = GCT, TGT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT,
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<222> (349)..(351)

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GTT or TAT

<400> 252

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 50 55 60

Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val
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Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
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 100 105 110

His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
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Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
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 145 150 155 160

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
 165 170 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
 180 185 190

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
 195 200 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
 210 215 220

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 245 250 255

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Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser
 275 280 285

Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
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Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser
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Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
 325 330 335

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
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Cys Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly
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Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
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Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
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Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
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Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
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Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Glu
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Phe Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala

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485

490

495

Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp Glu Asn Ala Leu
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Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly
 515 520 525

Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly Leu Ala Asn Gly
 530 535 540

Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser Gln Met Ala Gln
 545 550 555 560

Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr
 565 570 575

Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro Phe Val Phe Gly
 580 585 590

Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu
 595 600 605

Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr
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Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser
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<220>

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<400> 255

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cgtttttagcg gatccaaaag cggcaccagc gcgagccttg cgattacggg cctgcaaagc 240

gaagacgaag cggattatta ttgccagagc tatgacatgc ctcaggctgt gtttggcggc 300

ggcacgaagt ttaaccgttc ttggccagcc gaaagccgca ccgagtgtga cgctgtttcc 360

108/165

gccgagcagc gaagaattgc aggcgaacaa agcgaccctg gtgtgcctga ttagcgactt	420
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109/165

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110/165

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<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct

<400> 256

Ala Glu Phe Arg His Asp Cys

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<210> 257

<211> 7

<212> PRT

<213> artificial sequence

111/165

<220>
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<400> 257

Glu Phe Arg His Asp Ser Cys
1 5

<210> 258
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<213> artificial sequence

<220>
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<400> 258

Phe Arg His Asp Ser Gly Cys
1 5

<210> 259
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<220>
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<400> 259

Arg His Asp Ser Gly Tyr Cys
1 5

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<220>
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<400> 260

His Asp Ser Gly Tyr Glu Cys
1 5

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<220>
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112/165

<400> 261

Asp Ser Gly Tyr Glu Val Cys
1 5

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<211> 7

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<213> artificial sequence

<220>

<223> synthetic construct

<400> 262

Ser Gly Tyr Glu Val His Cys
1 5

<210> 263

<211> 7

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct

<400> 263

Tyr Glu Val His His Gln Cys
1 5

<210> 264

<211> 7

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct

<400> 264

Glu Val His His Gln Lys Cys
1 5

<210> 265

<211> 7

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<213> artificial sequence

<220>

<223> synthetic construct

<400> 265

Val His His Gln Lys Leu Cys

113/165

1

5

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<220>
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<400> 266

His His Gln Lys Leu Val Cys
1 5

<210> 267
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<220>
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<400> 267

His Gln Lys Leu Val Phe Cys
1 5

<210> 268
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<220>
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Gln Lys Leu Val Phe Phe Cys
1 5

<210> 269
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<220>
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<400> 269

Lys Leu Val Phe Phe Ala Cys
1 5

114/165

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<400> 270

Leu Val Phe Phe Ala Glu Cys
1 5

<210> 271
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<220>
<223> synthetic construct

<400> 271

Val Phe Phe Ala Glu Asp Cys
1 5

<210> 272
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Phe Phe Ala Glu Asp Val Cys
1 5

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<220>
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<400> 273

Phe Ala Glu Asp Val Gly Cys
1 5

<210> 274
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115/165

<213> artificial sequence

<220>

<223> synthetic construct

<400> 274

Ala Glu Asp Val Gly Ser Cys
1 5

<210> 275

<211> 7

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct

<400> 275

Glu Asp Val Gly Ser Asn Cys
1 5

<210> 276

<211> 7

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<213> artificial sequence

<220>

<223> synthetic construct

<400> 276

Asp Val Gly Ser Asn Lys Cys
1 5

<210> 277

<211> 7

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<213> artificial sequence

<220>

<223> synthetic construct

<400> 277

Val Gly Ser Asn Lys Gly Cys
1 5

<210> 278

<211> 7

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<220>

116/165

<223> synthetic construct

<400> 278

Gly Ser Asn Lys Gly Ala Cys
1 5

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<400> 279

Cys Ser Asn Lys Gly Ala Ile
1 5

<210> 280

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<220>

<223> synthetic construct

<400> 280

Cys Asn Lys Gly Ala Ile Ile
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<210> 281

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<213> artificial sequence

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<223> synthetic construct

<400> 281

Cys Lys Gly Ala Ile Ile Gly
1 5

<210> 282

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<213> artificial sequence

<220>

<223> synthetic construct

<400> 282

117/165

Cys Gly Leu Met Val Gly Gly
1 5

<210> 283
<211> 7
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<213> artificial sequence

<220>
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<400> 283

Cys Met Val Gly Gly Val Val
1 5

<210> 284
<211> 7
<212> PRT
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<220>
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<400> 284

Cys Gly Gly Val Val Ile Ala
1 5

<210> 285
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<220>
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<400> 285

Ala Glu Phe Arg His Asp
1 5

<210> 286
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<400> 286

Glu Phe Arg His Asp Ser Gly
1 5

118/165

<210> 287
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<220>
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<400> 287

Glu Phe Arg His Asp
1 5

<210> 288
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<400> 288

His Asp Ser Gly
1

<210> 289
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<220>
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<400> 289

His His Gln Lys Leu
1 5

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<213> artificial sequence

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<223> synthetic construct; peptide 6 A beta

<400> 290

Leu Val Phe Phe Ala Glu
1 5

<210> 291

119/165

<211> 6
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<220>
<223> synthetic construct; peptide 7 A beta

<400> 291

Val Phe Phe Ala Glu Asp
1 5

<210> 292
<211> 4
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<220>
<223> synthetic construct; peptide 8 A beta

<400> 292

Val Phe Phe Ala
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<210> 293
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; peptide 9 A beta

<400> 293

Phe Phe Ala Glu Asp Val
1 5

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<220>
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atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtct tactcattat 300

120/165

gctcgttatt atcggtattt tgatgtttgg ggccaaggca ccctggtgac ggtagctca 360

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<211> 120
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 295

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Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Val
35 40 45

Ile Ser Glu Lys Ser Arg Phe Ile Tyr Tyr Ala Asp Ser Val Lys Gly
50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65 70 75 80

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
85 90 95

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 296
<211> 360
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 296

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121/165

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 <213> artificial sequence

<220>
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<400> 297

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Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
 20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala
 35 40 45

Ile Ser Glu Thr Ser Ile Arg Lys Tyr Tyr Ala Asp Ser Val Lys Gly
 50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
 65 70 75 80

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
 85 90 95

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 298
 <211> 360
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 <213> artificial sequence

<220>
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122/165

<400> 298
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<210> 299
 <211> 120
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 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 299

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Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
 20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Val
 35 40 45

Ile Ser Gln Thr Gly Arg Lys Ile Tyr Tyr Ala Asp Ser Val Lys Gly
 50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
 65 70 75 80

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
 85 90 95

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 300
 <211> 360
 <212> DNA

123/165

<213> artificial sequence

<220>

<223> synthetic construct

<400> 300

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atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtct tactcattat      300
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<210> 301

<211> 120

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct

<400> 301

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Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
1           5           10           15

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Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
          20           25           30

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Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Val
35           40           45

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```

Ile Ser Gln Thr Gly Arg Lys Ile Tyr Tyr Ala Asp Ser Val Lys Gly
50           55           60

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Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65           70           75           80

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Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
          85           90           95

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Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val Trp Gly Gln
100           105           110

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Gly Thr Leu Val Thr Val Ser Ser
115           120

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124/165

<210> 302
 <211> 360
 <212> DNA
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<220>
 <223> synthetic construct

<400> 302
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 aagggctctcg agtgggtgag cgttatttct gagactggta agaataattta ttatgctgat 180
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<210> 303
 <211> 120
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 303

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
 1 5 10 15

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
 20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Val
 35 40 45

Ile Ser Glu Thr Gly Lys Asn Ile Tyr Tyr Ala Asp Ser Val Lys Gly
 50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
 65 70 75 80

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
 85 90 95

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val Trp Gly Gln

125/165

100

105

110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 304

<211> 360

<212> DNA

<213> artificial sequence

<220>

<223> synthetic construct

<400> 304

caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgcg tctgagctgc 60
 gcggcctccg gatttacctt tagcagctat gcgatgagct gggtgcgcca agcccctggg 120
 aagggctcgc agtgggtgag cgttatttct gagactggta agaataattta ttatgctgat 180
 tctgttaagg gtcgtttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240
 atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtct tactcattat 300
 gctcgttatt atcgttattt tgatgtttgg ggccaaggca ccctggtgac ggtagctca 360

<210> 305

<211> 120

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct

<400> 305

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
 1 5 10 15

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
 20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Val
 35 40 45

Ile Ser Glu Thr Gly Lys Asn Ile Tyr Tyr Ala Asp Ser Val Lys Gly
 50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
 65 70 75 80

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Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
 85 90 95

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 306
 <211> 360
 <212> DNA
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 306
 caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgcg tctgagctgc 60
 gcggcctccg gatttacctt tagcagctat gcgatgagct gggcgcgcca agcccctggg 120
 aaggggtctcg agtgggtgag cgctatttct gagtctggta agactaagta ttatgctgat 180
 tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240
 atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtct tactcattat 300
 gctcgttatt atcgttattt tgatgttttg ggccaaggca ccttggtgac ggtagctca 360

<210> 307
 <211> 120
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 307

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
 1 5 10 15

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
 20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala
 35 40 45

Ile Ser Glu Ser Gly Lys Thr Lys Tyr Tyr Ala Asp Ser Val Lys Gly
 50 55 60

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Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65 70 75 80

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
85 90 95

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 308
<211> 372
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 308
caattggtgg aaagcggcgg cggcctggtg caaccggggc gcagcctgcg tctgagctgc 60
gcggcctccg gatttacott tagcagctat gcgatgagct gggcgcgcca agcccctggg 120
aagggtctcg agtgggtgag cgctattaat ggtactggta tgaagaagta ttatgctgat 180
tctgttaagg gtcgtttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240
atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtgg taagggtaat 300
actcataagc cttatgggta tggtcggttat tttgatgttt ggggccaagg caccctgggtg 360
acggttagct ca 372

<210> 309
<211> 124
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 309

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
1 5 10 15

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
20 25 30

128/165

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala
 35 40 45

Ile Asn Gly Thr Gly Met Lys Lys Tyr Tyr Ala Asp Ser Val Lys Gly
 50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
 65 70 75 80

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
 85 90 95

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
 100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 310
 <211> 372
 <212> DNA
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 310
 caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgcg tctgagctgc 60
 gcggcctccg gatttacctt tagcagctat gcgatgagct gggcgcgcca agcccctggg 120
 aagggtctcg agtgggtgag cgctattaat tataatggtg ctogtattta ttatgctgat 180
 tctgttaagg gtcgttttac catttcacgt gataattoga aaaacaccct gtatctgcaa 240
 atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtgg taagggtaat 300
 actcataagc cttatgggta tgttcgttat ttgatgttt ggggccaagg caccctggtg 360
 acggttagct ca 372

<210> 311
 <211> 124
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 311

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu

1				5					10						15	
Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Ala	Met	
			20					25					30			
Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ser	Ala	
		35					40					45				
Ile	Asn	Tyr	Asn	Gly	Ala	Arg	Ile	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	
	50					55					60					
Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	
65					70					75					80	
Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	
				85					90					95		
Gly	Lys	Gly	Asn	Thr	His	Lys	Pro	Tyr	Gly	Tyr	Val	Arg	Tyr	Phe	Asp	
			100					105					110			
Val	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser					
		115					120									

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<220>
<223> synthetic construct
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<400>	312
caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgcg tctgagctgc	60
gcggcctccg gatttacctt tagcagctat gcgatgagct gggtgcgcca agcccctggg	120
aagggtctcg agtgggtgag cgctattaat gctgatggta atcgtaahta ttatgctgat	180
tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa	240
atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtgg taagggtaat	300
actcataagc cttatggtta tgttcgttat tttgatgttt ggggccaaagg caccctgggtg	360
acgggttagct ca	372

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<210> 313
<211> 124
<212> PRT
<213> artificial sequence
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130/165

<220>

<223> synthetic construct

<400> 313

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
 1 5 10 15

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
 20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala
 35 40 45

Ile Asn Ala Asp Gly Asn Arg Lys Tyr Tyr Ala Asp Ser Val Lys Gly
 50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
 65 70 75 80

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
 85 90 95

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
 100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 314

<211> 372

<212> DNA

<213> artificial sequence

<220>

<223> synthetic construct

<400> 314

caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgog tctgagctgc 60
 ggggcctccg gatttacctt tagcagctat gcgatgagct gggcgccca agccctggg 120
 aagggtctcg agtgggtgag cgctattaat gctgatggta atcgtaagta ttatgctgat 180
 tctgttaagg gtcgttttac catttcacgt gataattoga aaaacaccct gtatctgcaa 240
 atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtgg taagggtaat 300
 actcataagc cttatgggta tgttcgttat ttgatgttt ggggccaagg caccctgggtg 360

131/165

acggttagct ca

372

<210> 315
 <211> 124
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 315

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
 1 5 10 15

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
 20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala
 35 40 45

Ile Asn Ala Asp Gly Asn Arg Lys Tyr Tyr Ala Asp Ser Val Lys Gly
 50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
 65 70 75 80

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
 85 90 95

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
 100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 316
 <211> 372
 <212> DNA
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 316
 caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgcg tctgagctgc 60
 gcggcctccg gatttacctt tagcagctat gcgatgagct gggcgcgcca agcccctggg 120
 aagggtctcg agtgggtgag cgctattaat gctaattggtt ataagaagta ttatgctgat 180

132/165

tctgttaagg gtcgtttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240
 atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtgg taagggtaat 300
 actcataagc cttatgggta tgttcgttat tttgatgttt ggggcccaagg caccctgggtg 360
 acggttagct ca 372

<210> 317
 <211> 124
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 317

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
 1 5 10 15

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
 20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala
 35 40 45

Ile Asn Ala Asn Gly Tyr Lys Lys Tyr Tyr Ala Asp Ser Val Lys Gly
 50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
 65 70 75 80

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
 85 90 95

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
 100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 318
 <211> 372
 <212> DNA
 <213> artificial sequence

<220>
 <223> synthetic construct

133/165

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<400> 318
caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgcg tctgagctgc      60
gcggcctccg gatttacctt tagcagctat gcgatgagct gggtgcgcca agcccctggg      120
aagggtctcg agtgggtgag cgctattaat gctaattggtt ataagaagta ttatgctgat      180
tctgttaagg gtcgtttttac catttcacgt gataattoga aaaacaccct gtatctgcaa      240
atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtgg taagggtaat      300
actcataagc cttatgggta tgttcgttat tttgatgttt ggggcccaagg caccctggtg      360
acggttagct ca                                                                372

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<210> 319
<211> 124
<212> PRT
<213> artificial sequence

```

```

<220>
<223> synthetic construct

```

```

<400> 319

```

```

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
1           5           10           15

```

```

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
          20           25           30

```

```

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala
    35           40           45

```

```

Ile Asn Ala Asn Gly Tyr Lys Lys Tyr Tyr Ala Asp Ser Val Lys Gly
    50           55           60

```

```

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
    65           70           75           80

```

```

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
          85           90           95

```

```

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
    100           105           110

```

```

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
    115           120

```

134/165

<210> 320
 <211> 372
 <212> DNA
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 320
 caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgcg tctgagctgc 60
 gcggcctccg gatttacott tagcagctat gcgatgagct gggcgcgcca agcccctggg 120
 aagggctctcg agtgggtgag cgctattaat gctaattggtt ataagaagta ttatgctgat 180
 tctgttaagg gtcgtttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240
 atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtgg taagggtaat 300
 actcataagc cttatgggta tggttcgttat tttgatgttt ggggcccaagg caccctggtg 360
 acggtttagct ca 372

<210> 321
 <211> 124
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 321

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
 1 5 10 15

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
 20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala
 35 40 45

Ile Asn Ala Asn Gly Tyr Lys Lys Tyr Tyr Ala Asp Ser Val Lys Gly
 50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
 65 70 75 80

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
 85 90 95

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp

135/165

100

105

110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 322
 <211> 366
 <212> DNA
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 322
 caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgcg tctgagctgc 60
 gcggcctccg gatttacctt tagcagctat gcgatgagct ggggtgcgcca agcccctggg 120
 aagggctctcg agtgggtgag cgctatttct cgttctgggtt ctaatattta ttatgctgat 180
 tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240
 atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtct tctttctcgt 300
 gggtataatg gttattatca taagtttgat gtttggggcc aaggcaccct ggtgacggtt 360
 agctca 366

<210> 323
 <211> 122
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 323

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
 1 5 10 15

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
 20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala
 35 40 45

Ile Ser Arg Ser Gly Ser Asn Ile Tyr Tyr Ala Asp Ser Val Lys Gly
 50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
 65 70 75 80

136/165

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
 85 90 95

Leu Leu Ser Arg Gly Tyr Asn Gly Tyr Tyr His Lys Phe Asp Val Trp
 100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 324
 <211> 330
 <212> DNA
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 324
 gatatcgtgc tgaccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60
 ctgagctgca gagcgagccg gcgtattcat gtttattatc tggcgtggta ccagcagaaa 120
 ccaggtcaag caccgcgtct attaatattat ggcgcgagca gccgtgcaac tgggggtcccg 180
 gcgcgtttta gcggctcttg atccggcacg gattttaccc tgaccattag cagcctggaa 240
 cctgaagact ttgcgaacta ttattgccag cagacttatg attatcctcc tacctttggc 300
 cagggtacga aagttgaaat taaacgtacg 330

<210> 325
 <211> 110
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 325

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Arg Arg Ile His Val Tyr
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser

137/165

50

55

60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Asp Tyr Pro
85 90 95

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 326
<211> 330
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 326
gatatcgtgc tgaccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60
ctgagctgca gagcgagccg gcgtattcat gtttattatc tggcgtggta ccagcagaaa 120
ccaggtcaag caccgcgtct attaatattat ggcgcgagca gccgtgcaac tgggggtccc 180
gcgcgtttta gcggctcttg atccggcacg gattttaccc tgaccattag cagcctggaa 240
cctgaagact ttgcgactta ttattgccag cagacttatg attatcctcc tacctttggc 300
cagggtagca aagttgaaat taaacgtacg 330

<210> 327
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 327

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Arg Arg Ile His Val Tyr
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

138/165

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Asp Tyr Pro
 85 90 95

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
 100 105 110

<210> 328
 <211> 330
 <212> DNA
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 328
 gatatacgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60
 ctgagctgca gagcgagcca gcgtcttggt cgtctttatc tggcgtggta ccagcagaaa 120
 ccagggtcaag caccgcgtct attaatattat ggcgcgagca gccgtgcaac tgggggtcccg 180
 gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240
 cctgaagact ttgcgactta ttattgccag cagacttatg attatcctcc tacctttggc 300
 cagggtagca aagttgaaat taaacgtacg 330

<210> 329
 <211> 110
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 329

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Leu Gly Arg Leu
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

139/165

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Asp Tyr Pro
 85 90 95

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
 100 105 110

<210> 330
 <211> 330
 <212> DNA
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 330
 gatatcgtgc tgaccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60
 ctgagctgca gagcgagccg gcgtattcat gtttattatc tggcgtggta ccagcagaaa 120
 ccaggtcaag caccgcgtct attaatattat ggcgcgagca gccgtgcaac tgggggtcccg 180
 gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240
 cctgaagact ttgcgactta ttattgccag cagacttatg attatcctcc tacctttggc 300
 caggggtacga aagttgaaat taaacgtacg 330

<210> 331
 <211> 110
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 331

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Arg Arg Ile His Val Tyr
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

140/165

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Asp Tyr Pro
 85 90 95

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
 100 105 110

<210> 332
 <211> 330
 <212> DNA
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 332
 gatatcgtgc tgaccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60
 ctgagctgca gagcgagccg gcgtattcat gtttattatc tggcgtggta ccagcagaaa 120
 ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tgggggtcccg 180
 gcgcgtttta gcggctctgg atccggcgcg gattttaccc tgaccattag cagcctggaa 240
 cctgaagact ttgcgactta ttattgccag cagacttatg attatcctcc tacctttggc 300
 cagggtacga aagttgaaat taaacgtacg 330

<210> 333
 <211> 110
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 333

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Arg Arg Ile His Val Tyr
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

141/165

35

40

45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Asp Tyr Pro
85 90 95

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 334

<211> 330

<212> DNA

<213> artificial sequence

<220>

<223> synthetic construct

<400> 334

gatatcgtgc tgaccagag cccggcgacc ctgagcctgt ctccggggcga acgtgcgacc 60
ctgagctgca gagcgagcca gcgtcttggt cgtctttatc tggcgtggta ccagcagaaa 120
ccaggtcaag caccgctctc attaatttat ggcgcgagca gccgtgcaac tgggggtccc 180
gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240
cctgaagact ttgcgactta ttattgccag cagacttatg attatcctcc tacctttggc 300
cagggtacga aagttgaaat taaacgtacg 330

<210> 335

<211> 110

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct

<400> 335

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Leu Gly Arg Leu
20 25 30

142/165

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Asp Tyr Pro
85 90 95

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 336
<211> 330
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 336
gatatcgtgc tgaccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60
ctgagctgca gagcgagcca gtttattcag cgtttttatc tggcgtggta ccagcagaaa 120
ccagggtcaag caccgctctc attaatattat ggcgcgagca gccgtgcaac tgggggtcccg 180
gcgcggtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240
cctgaagact ttgcggttta ttattgccag cagacttata attatcctcc tacctttggc 300
cagggtacga aagttgaaat taaacgtacg 330

<210> 337
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 337

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Phe Ile Gln Arg Phe
20 25 30

143/165

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Thr Tyr Asn Tyr Pro
85 90 95

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 338

<211> 330

<212> DNA

<213> artificial sequence

<220>

<223> synthetic construct

<400> 338

gatatcgtgc tgacccagaq cccggcgacc ctgagcctgt ctccggggcga acgtgcgacc 60

ctgagctgca gagcgagcca gtatgttgat cgtacttata tggcgtggta ccagcagaaa 120

ccagggtcaag caccgcgtct attaatattat ggcgcgagca gccgtgcaac tgggggtcccg 180

gcgcgtttta gcggtctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240

cctgaagact ttgcgactta ttattgccag cagatttatt cttttcctca tacctttggc 300

cagqgtacga aagttgaaat taaacgtacg 330

<210> 339

$\langle 211 \rangle$ 110

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct

<400> 339

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Tyr Val Asp Arg Thr
20 25 30

144/165

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ile Tyr Ser Phe Pro
 85 90 95

His Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
 100 105 110

<210> 340
 <211> 330
 <212> DNA
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 340
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 ctgagctgca gagcgagcca gcgttttttt tataagtatc tggcgtggta ccagcagaaa 120
 ccaggtcaag caccgcgtct attaatctct ggttcttcta accgtgcaac tgggggtcccg 180
 gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240
 cctgaagact ttgcggttta ttattgcctt cagctttata atattcctaa tacctttggc 300
 cagggtagca aagttgaaat taaacgtacg 330

<210> 341
 <211> 110
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 341

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Phe Phe Tyr Lys

145/165

20

25

30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Ser Gly Ser Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln Leu Tyr Asn Ile Pro
 85 90 95

Asn Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
 100 105 110

<210> 342
 <211> 330
 <212> DNA
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 342
 gatatcgtgc tgaccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60
 ctgagctgca gagcgagcca gtatgttgat cgtacttatac tggcgtggta ccagcagaaa 120
 ccagggtcaag caccgcgtct attaatattat ggcgcgagca gccgtgcaac tgggggtccc 180
 gcgcgtttta gcggctcttg atccggcacg gattttaccc tgaccattag cagcctggaa 240
 cctgaagact ttgcgactta ttattgccag cagatttatt cttttcctca tacctttggc 300
 cagggtacga aagttgaaat taaacgtacg 330

<210> 343
 <211> 110
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 343

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

146/165

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Tyr Val Asp Arg Thr
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ile Tyr Ser Phe Pro
 85 90 95

His Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
 100 105 110

<210> 344
 <211> 330
 <212> DNA
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 344
 gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60
 ctgagctgca gagcgagcca gtatgttttt cgtcgttatc tggcgtggta ccagcagaaa 120
 ccagggtcaag caccgcgtct attaatttct ggttcttcta accgtgcaac tgggggtcccg 180
 gcgcgtttta gcggctctgg atccggcacg gattttacco tgaccattag cagcctggaa 240
 cctgaagact ttgcggttta ttattgcctt cagctttata atattcctaa tacctttggc 300
 cagggtacga aagttgaaat taaacgtacg 330

<210> 345
 <211> 110
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 345

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

147/165

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Tyr Val Phe Arg Arg
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Ser Gly Ser Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln Leu Tyr Asn Ile Pro
85 90 95

Asn Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 346
<211> 330
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 346
gatatcgtgc tgaccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60
ctgagctgca gagcgagcca gtatgttgat cgtacttatc tggcgtggta ccagcagaaa 120
ccaggtcaag caccgctctc attaatattat ggccgcgagca gccgtgcaac tgggggtcccg 180
gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240
cctgaagact ttgcgactta ttattgccag cagatttatt cttttcctca tacctttggc 300
cagggtacga aagttgaaat taaacgtacg 330

<210> 347
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 347

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

148/165

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Tyr Val Asp Arg Thr
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ile Tyr Ser Phe Pro
 85 90 95

His Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
 100 105 110

<210> 348
 <211> 330
 <212> DNA
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 348
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 ctgagctgca gagcgagcca gcgtctttct cctcgttatc tggcgtggta ccagcagaaa 120
 ccaggtcaag caccgctctc attaatattat ggcgcgagca gccgtgcaac tgggggtcccg 180
 gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240
 cctgaagact ttgcgactta ttattgcott cagatttata atatgcctat tacctttggc 300
 cagggtacga aagttgaaat taaacgtacg 330

<210> 349
 <211> 110
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 349

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly

149/165

1					5					10					15				
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Arg	Leu	Ser	Pro	Arg				
			20					25					30						
Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu				
		35					40					45							
Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Val	Pro	Ala	Arg	Phe	Ser				
	50					55					60								
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Glu				
65					70					75					80				
Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Leu	Gln	Ile	Tyr	Asn	Met	Pro				
				85					90					95					
Ile	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr						
			100					105					110						

<210>	350
<211>	330
<212>	DNA
<213>	artificial sequence

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<220>
<223> synthetic construct
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[illegible]

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<210> 351
<211> 110
<212> PRT
<213> artificial sequence
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<220>
<223> synthetic construct
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<400> 351

150/165

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Tyr Val Phe Arg Arg
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Ser Gly Ser Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln Leu Tyr Asn Ile Pro
85 90 95

Asn Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 352
<211> 330
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 352
gatatcgtgc tgaccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60
ctgagctgca gagcgagcca gcgtgtttct ggctcgttatc tggcgtggta ccagcagaaa 120
ccagggtcaag caccgcgtct attaatattat ggcgcgagca gccgtgcaac tgggggtcccg 180
gcgcgtttta gcggctctgg atccggcaag gatatttacc tgaccattag cagcctggaa 240
cctgaagact ttgcgactta ttattgccag cagctttctt cttatcctcc tacctttggc 300
cagggtacga aagttgaaat taaacgtacg 330

<210> 353
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 353

151/165

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Val Ser Gly Arg
 20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
 50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
 65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Ser Ser Tyr Pro
 85 90 95

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
 100 105 110

<210> 354

<211> 39

<212> DNA

<213> artificial sequence

<220>

<223> synthetic construct

<400> 354

cttactcatt atgctcgta ttatcgttat ttgatgtt

39

<210> 355

<211> 13

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct

<400> 355

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val
 1 5 10

<210> 356

<211> 39

<212> DNA

<213> artificial sequence

152/165

<220>

<223> synthetic construct

<400> 356

cttactcatt atgctcggtta ttatcggttat tttgatggt

39

<210> 357

<211> 13

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct

<400> 357

Leu	Thr	His	Tyr	Ala	Arg	Tyr	Tyr	Arg	Tyr	Phe	Asp	Val
1				5					10			

<210> 358

<211> 39

<212> DNA

<213> artificial sequence

<220>

<223> synthetic construct

<400> 358

cttactcatt atgctcggtta ttatcggttat tttgatggt

39

<210> 359

<211> 13

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct

<400> 359

Leu	Thr	His	Tyr	Ala	Arg	Tyr	Tyr	Arg	Tyr	Phe	Asp	Val
1				5					10			

<210> 360

<211> 39

<212> DNA

<213> artificial sequence

<220>

<223> synthetic construct

<400> 360

cttactcatt atgctcggtta ttatcggttat tttgatggt

39

153/165

<210> 361
<211> 13
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 361

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val
1 5 10

<210> 362
<211> 39
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 362
cttactcatt atgctcgta ttatcggtat tttgatgtt 39

<210> 363
<211> 13
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 363

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val
1 5 10

<210> 364
<211> 39
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 364
cttactcatt atgctcgta ttatcggtat tttgatgtt 39

<210> 365
<211> 13
<212> PRT
<213> artificial sequence

<220>

154/165

<223> synthetic construct

<400> 365

Leu	Thr	His	Tyr	Ala	Arg	Tyr	Tyr	Arg	Tyr	Phe	Asp	Val
1				5					10			

<210> 366

<211> 39

<212> DNA

<213> artificial sequence

<220>

<223> synthetic construct

<400> 366

cttactcatt atgctcggtta ttatcggttat tttgatggt

39

<210> 367

<211> 13

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct

<400> 367

Leu	Thr	His	Tyr	Ala	Arg	Tyr	Tyr	Arg	Tyr	Phe	Asp	Val
1				5					10			

<210> 368

<211> 51

<212> DNA

<213> artificial sequence

<220>

<223> synthetic construct

<400> 368

ggtaagggtta atactcataa gccttatggt tatgttcggt attttgatgt t

51

<210> 369

<211> 17

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct

<400> 369

Gly	Lys	Gly	Asn	Thr	His	Lys	Pro	Tyr	Gly	Tyr	Val	Arg	Tyr	Phe	Asp
1				5					10					15	

155/165

Val

<210> 370
<211> 51
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 370
ggtaagggtataactcataa gccttatgggtatgttcggtatgttgatgt t 51

<210> 371
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 371
Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
1 5 10 15

Val

<210> 372
<211> 51
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 372
ggtaagggtataactcataa gccttatgggtatgttcggtatgttgatgt t 51

<210> 373
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 373
Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
1 5 10 15

156/165

Val

<210> 374
<211> 51
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 374
ggtaagggtataactcataa gccttatgggtatgttcggtatgttgatgt t 51

<210> 375
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 375
Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
1 5 10 15

Val

<210> 376
<211> 51
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 376
ggtaagggtataactcataa gccttatgggtatgttcggtatgttgatgt t 51

<210> 377
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 377
Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp

157/165

1 5 10 15

Val

<210> 378
<211> 51
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 378
ggtaagggtataactcataa gccttatggt tatgttcggt attttgatgt t 51

<210> 379
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 379

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
1 5 10 15

Val

<210> 380
<211> 51
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 380
ggtaagggtataactcataa gccttatggt tatgttcggt attttgatgt t 51

<210> 381
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 381

158/165

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
 1 5 10 15

Val

<210> 382
 <211> 45
 <212> DNA
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 382
 cttctttctc gtggttataa tggttattat cataagtttg atggt

45

<210> 383
 <211> 15
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 383

Leu Leu Ser Arg Gly Tyr Asn Gly Tyr Tyr His Lys Phe Asp Val
 1 5 10 15

<210> 384
 <211> 24
 <212> DNA
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 384
 cagcagactt atgattatcc tcct

24

<210> 385
 <211> 8
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic construct

<400> 385

Gln Gln Thr Tyr Asp Tyr Pro Pro
 1 5

159/165

<210> 386
<211> 24
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 386
cagcagactt atgattatcc tcct

24

<210> 387
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 387

Gln Gln Thr Tyr Asp Tyr Pro Pro
1 5

<210> 388
<211> 24
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 388
cagcagactt atgattatcc tcct

24

<210> 389
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 389

Gln Gln Thr Tyr Asp Tyr Pro Pro
1 5

<210> 390
<211> 24
<212> DNA
<213> artificial sequence

<220>

160/165

<223> synthetic construct

<400> 390

cagcagactt atgattatcc tcct

24

<210> 391

<211> 8

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct

<400> 391

Gln Gln Thr Tyr Asp Tyr Pro Pro
1 5

<210> 392

<211> 24

<212> DNA

<213> artificial sequence

<220>

<223> synthetic construct

<400> 392

cagcagactt atgattatcc tcct

24

<210> 393

<211> 8

<212> PRT

<213> artificial sequence

<220>

<223> synthetic construct

<400> 393

Gln Gln Thr Tyr Asp Tyr Pro Pro
1 5

<210> 394

<211> 24

<212> DNA

<213> artificial sequence

<220>

<223> synthetic construct

<400> 394

cagcagactt atgattatcc tcct

24

<210> 395

161/165

<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 395

Gln Gln Thr Tyr Asp Tyr Pro Pro
1 5

<210> 396
<211> 24
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 396
cagcagactt ataattatcc tcct

24

<210> 397
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 397

Gln Gln Thr Tyr Asn Tyr Pro Pro
1 5

<210> 398
<211> 24
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 398
cagcagattt attcttttcc tcat

24

<210> 399
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

162/165

<400> 399

Gln Gln Ile Tyr Ser Phe Pro His
1 5

<210> 400

<211> 24

<212> DNA

<213> artificial sequence

<220>

<223> synthetic construct

<400> 400

cttcagcttt ataattattcc taat

24

<210> 401

<211> 8

<212> PRT

<213> artificial sequence

<220>

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163/165

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Glu Val His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser
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Asn Lys Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala
35 40 45

Thr Val Ile Val
50